





Query Match	Score	DB	Length
Best Local Similarity	46.48		
Matches	150	Conservative	0
		Mismatches	173
		Indels	0
		Gaps	0

  

QY	96	CTGACCGCCGAGAGGAGCTCAAGAGTTCAAGCTGAAGCTGCTGCGGTGCGGCGGAG	155
10632	CTGAGCAGCGCGCTGTGATTAACGCGCTTCGACGTCAGCGCGCACCTGTGGCTGGCGCGCAG	10691	



Query Match	6.0%;	Score 44.6;	DB 4;	Length 15079;
Best Local Similarity	47.6%;	Pred. No. 0.28;		
Matches 131; Conservative	0;	Mismatches 144;	Indels 0;	Gaps 0;

QY	69	GACCCATCTCTGGATGCGGTGGAGAACCTGACCGCGAGACCTCAAGATTCACGCTG	128
Db	1092	GTCGTGATCTCTGGACCGCTGATGTCGCCGCCAGCTGCTGTCAMACACTACCGGCTTCAAGGAC	1033
QY	129	AAGCTGCTGTGCGGTGCGCTGTCCGCGAGGGCTCTACGGGCGCATCCCGGGGCGCGCTGCTG	188
Db	1032	ACGGAGGGCAAGCGGGGTGAAGACACACTATCGACCGCGGGTCTCAAGTCCGCCGCCCGCGCG	973
QY	189	TCCATGGAGGCTCTGGAGCCCTCACCCGACAGTGCAGTCTTCTTACTCTGAGAACCTACGGC	248
Db	972	GCCCTGGAGGGCTCTGAGAGAAAGACGGCGGATGTGCGCTGTGACCCCGCCACCGGCGAAC	913
QY	249	GCCGAGCTCACCGCTAACCTGTGCGCGCATGTGGGCGTTCAGAGAGATGGCGGGCAGCTG	308
Db	912	ATCTGTGCGCCGCGCGAAGCGCCCTCCGGCATGAAACCGCGGCGCTGAGAGGCGGTACCG	853
Y	309	CAGGCGGCGACGACACAGGGCTCTGGAGCGCGGGCC	343
Db	852	CCCGGCTCACCTTCAAGGGGTGCACACACCGCGGC	818

RESULT 9  
US-08-911-853-6

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: Sequence 6, Application US/08911853
: Patent No. 6048710
:
: GENERAL INFORMATION:
: APPLICANT: Gerltse, Gijshert
: APPLICANT: Quax, Wilhelmus J.
: TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
: TITLE OF INVENTION: EXPRESSION LEVELS
: NUMBER OF SEQUENCES: 37
: CORRESPONDENCE ADDRESS:
: ADDRESSEE: Genecore International
: STREET: 925 Page Mill Road
: CITY: Palo Alto
: STATE: CA
: COUNTRY: USA
: ZIP: 94304-1013
: COMPUTER READABLE FORM:
: MEDIUM TYPE: Diskette
: COMPUTER: IBM Compatible
: OPERATING SYSTEM: DOS
: SOFTWARE: FastSeq for Windows Version 2.0
:
: CURRENT APPLICATION DATA:
: APPLICATION NUMBER: US/08/911,853
: FILING DATE:
:
: PRIOR APPLICATION DATA:
: APPLICATION NUMBER: 08/659,092
: FILING DATE: 16-AUG-1996
: ATTORNEY/AGENT INFORMATION:
: NAME: Galtier, Debra J
: REGISTRATION NUMBER: 33,888
: REFERENCE/DOCKET NUMBER: GC361-2
: TELECOMMUNICATION INFORMATION:
: TELEPHONE: 650-846-7620
: TELEFAX: 650-845-6504
:
: INFORMATION FOR SEQ ID NO: 6:
: SEQUENCE CHARACTERISTICS:
: LENGTH: 1512 base pairs
: TYPE: nucleic acid
: STRANDEDNESS: single
: TOPOLOGY: linear
:
: IS-08-911-853-6

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Query Match	6.0%	Score 44.4	DB 3	Length 1512
Best Local Similarity	52.1%	Pred. No. 0.19		
Matches 124	Conservative	0	Mismatches 111	Indels 3
				Gaps 1
53	CATGGGGGGGGGGGGCCGACCTTCCTTGAGNAACTTGACCGCGGAGAGCT	112		

Db	894	CTTGGAAAGCATGGCCAGACCCAGGTCAACCCGCGGGTGGACATGACTTGTGCCCGCG	953
Qy	113	CAAGAAATTCAAGCTGAAGTGTCTGTGCGTGCCTGCGTGCAGAGGCTATCGGCGCATCC	172
Db	954	CTCTGCGGCCATCTCTGGCCAGGACCCGGACGTGGTGGATGGTGTGGGCGAGATCCGGACCA	1013
Qy	173	GGCGGGCGCGCTCTGTCCATGTGACCGCTTTGGACCTCAACCGCAAGCTGTGTAGCTTTCA	232
Db	1014	GGAGACCGCGCGAATGCGCTGTGCAAGGCTCTG---CTCAACCGGCGCACTGTGTCTTCCAC	1070
Qy	233	CTTGGAGACCTACGGGCGCAGGCTCAACCGCTAAACGHTGCCTGCAATGGCGCTCAG	290
Db	1071	CTCTGCAACCAAGCGCGGTGTGGCGCGCTCAACCGGCTGTGTGTGACATGGCGTGTGAG	1128

RESULT 10  
US-09-479-409-6

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Query Match	6.08;	Score 44.4;	DB 4;	Length 1512;
Best Local Similarly	52.18;	Pred. No. 0.19;		
Matches 124; Conservative	0;	Mismatches 111;	Indels 3;	Gaps 1;

QY	53	CATGGGCGGGCGGAGACCCATCTCGGATGGCGGTGGGAACCTCGACGCCGAGAGACT	112
Db	894	CTTGGAGGCGATGGCGCCAGCCAGSTCAACCCGCGGTGGCAATGACTCTTGCCCGCGG	953
QY	113	CAGAGTTCAGACTGAAGTGTGCTGTGGGTGGCGCTGCGCGAGGGCTACGGGCGCATCCC	172
Db	954	CTGTCCGGCGCATCTCTGGCGCAGGACCCGGAGCTGGTGATGTCTGGCGAGATCCGGGACCA	1013
QY	173	GCGGGGCGGCTGTCTGCATGGAGCCCTTGGAGCTCAACCGACAAAGTGGTACGTTCTA	232

Mon Dec 16 07:22:18 2002

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Page 6

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Db 1014 GGAGACGGCGGACATCGCGGTGAGGCGCTCG--CTCACCGGCCACCTGTCTCTCCAC 1070
QY 233 CTTGGAGACCTAGCGCGGCGGACCTGACCGGCAACGTCGTCGGGACATGCGGCGGCGGCGAG 290
Db 1071 CTTGGACACCAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1128

RESULT 11
US-09-479-453-6
/ Sequence 6, Application US/09479453
/ Patent No. 6313283
/ GENERAL INFORMATION:
/ APPLICANT: Geritise, Gijbert
/ APPLICANT: Quax, Wilhelms J.
/ TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
/ TITLE OF INVENTION: EXPRESSION LEVELS
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
/ ADDRESSEE: Genencor International
/ STREET: 925 Page Mill Road
/ CITY: Palo Alto
/ STATE: CA
/ COUNTRY: USA
/ ZIP: 94304-1013
/ COMPUTER READABLE FORM:
/ MEDIUM TYPE: Diskette
/ OPERATING SYSTEM: DOS
/ SOFTWARE: FASTSEQ FOR Windows Version 2.0
/ CURRENT APPLICATION DATA:
/ APPLICATION NUMBER: US/09/479,453
/ FILING DATE:
/ PRIOR APPLICATION DATA:
/ APPLICATION NUMBER: 08/911,853
/ FILING DATE:
/ ATTORNEY/AGENT INFORMATION:
/ NAME: Gjalster, Debra J.
/ REGISTRATION NUMBER: 3,888
/ REFERENCE/DOCKET NUMBER: GC361-2
/ TELECOMMUNICATION INFORMATION:
/ TELEPHONE: 650-845-7620
/ TELEFAX: 650-845-6504
/ INFORMATION FOR SEQ ID NO:
/ SEQUENCE CHARACTERISTICS:
/ LENGTH: 1512 base pairs
/ TYPE: nucleic acid
/ STRANDEDNESS: single
/ TOPOLOGY: linear
/
US-09-479-453-6

Query Match
Best Local Similarity 52.1%; Score 44.4; DB 4; Length 1512;
Matches 124; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

Db 53 CATGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 112
Db 894 CTTGGAAGGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 953
QY 113 CAAGAAGTTCAAGCTGAGCTGCTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 172
Db 954 CTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 172
QY 173 GCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1013
Db 1014 GGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 232
QY 233 CTTGGAGACCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1070
Db 1071 CTTGGACACCAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 1128

RESULT 12
US-08-911-853-29

Sequence 29, Application US/08911853
Patent No. 6048710
GENERAL INFORMATION:
APPLICANT: Geritise, Gijbert
APPLICANT: Quax, Wilhelms J.
TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
TITLE OF INVENTION: EXPRESSION LEVELS
NUMBER OF SEQUENCES: 37
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genencor International
STREET: 925 Page Mill Road
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304-1013
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ FOR Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/911,853
FILING DATE:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/699,092
FILING DATE: 16-AUG-1996
ATTORNEY/AGENT INFORMATION:
NAME: Gjalster, Debra J.
REGISTRATION NUMBER: 3,888
REFERENCE/DOCKET NUMBER: GC361-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 650-845-7620
TELEFAX: 650-845-6504
INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
LENGTH: 17612 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
US-08-911-853-29

Query Match
Best Local Similarity 52.1%; Score 44.4; DB 3; Length 17612;
Matches 124; Conservative 0; Mismatches 111; Indels 3; Gaps 1;

QY 53 CATGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 112
Db 11015 CTTGGAAGGATCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11074
QY 113 CAAGAAGTTCAAGCTGAGCTGCTGTGCTGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 172
Db 11075 CTTGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 172
QY 173 GCGGGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11134
Db 11135 GGAGACCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 232
QY 233 CTTGGAGACCTAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11191
Db 11192 CTTGGACACCAACAGCGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 11249

RESULT 13
US-09-479-409-29
/ Sequence 29, Application US/09479409
/ Patent No. 6225106
/ GENERAL INFORMATION:
/ APPLICANT: Geritise, Gijbert
/ APPLICANT: Quax, Wilhelms J.
/ TITLE OF INVENTION: EXPRESSION SYSTEM FOR ALTERED
/ TITLE OF INVENTION: EXPRESSION LEVELS
/ NUMBER OF SEQUENCES: 37
/ CORRESPONDENCE ADDRESS:
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? OPERATING SYSTEM: DOS
? SOFTWARE: FastSeq for Windows Version 2.0
? CURRENT APPLICATION DATA:
? APPLICATION NUMBER: US/09/479,453
? FILING DATE:
? PRIOR APPLICATION DATA:
? APPLICATION NUMBER: 08/911,853
? FILING DATE:
? ATTORNEY/AGENT INFORMATION:
? NAME: Gjalster, Debra J
? REGISTRATION NUMBER: 33,888
? REFERENCE/DOCKET NUMBER: GC361-2
? TELECOMMUNICATION INFORMATION:
? TELEPHONE: 650-846-7620
? TELEFAX: 650-845-6504
? INFORMATION FOR SEQ ID NO: 29:
? SEQUENCE CHARACTERISTICS:
? LENGTH: 17612 base pairs
? TYPE: nucleic acid
? STRANDEDNESS: single
? TOPOLOGY: linear
? OS-09-479-453-29

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Query Match	5.0%;	Score 44.4;	DB 4;	Length 17612;
Best Local Similarity	52.1%;	Pred. No. 0.32;		
Matches	124;	Conservative	0;	Mismatches 111; Indels 3; Gaps 1;
QY	53	CATGGGCGCGCGCGCGAGCCCATCTTGATGCGCTGGAGAACTGACCGCCGAGAGACT	112	
Db	11015	CCTGGAAGGCGATCGCGCCAGACCCAGTGCAACCCGCGGGGACATGCTTCCTGCGCGG	11074	
QY	113	CAAGAAGTTCAGAGCGGAGAGCTGTGTGGTGCGCTGGGCGAGGGGCTACGGGCGCATGCC	172	
Db	11075	CCTGCGCGCCCATCTCGCGCCAGACCCGAGCTGTGTGATGTGTGGCGAGATCCGCGACCA	11134	
QY	173	GCGGGCGCGCTGTCTGTCCATGAGACGCGCTTGACCTACCGACAAGCTGTGACGTTCTTA	232	
Db	11135	GGAGACCCGCCGACATCGCGCTGACAGGCGCTCG---CTCACCGGCGCACCTGTCTCTCCAC	11191	
QY	233	CCTGGAGACCTTAACGGCGCGGAGCTACACCGCTAACGTGTGGCGCGAGACGGGCGTCGAG	290	
Db	11192	CTGTGACCCCAACAGCGCGCTGTGGGCGCGTCAACCGCGCTGTGTGACATGGGCGTGAAG	11249	

RESULT 15  
US-08-845-998-7  
Sequence 7, Application US/08845998  
Patent No. 5879892  
GENERAL INFORMATION:  
APPLICANT: Van Baren, Nicolas  
APPLICANT: Coulle, Pierre G.  
APPLICANT: De Smet, Charles  
APPLICANT: Lucas, Sophie  
APPLICANT: Boon, Thierry  
TITLE OF INVENTION: LEUKEMIA ASSOCIATED GENES  
NUMBER OF SEQUENCES: 16  
CORRESPONDENCE ADDRESS:  
ADDRESSEE: Wolf, Greenfield & Sacks, P.C.  
STREET: 600 Atlantic Avenue  
CITY: Boston  
STATE: MA  
COUNTRY: US  
ZIP: 02210  
COMPUTER READABLE FORM:  
MEDIUM TYPE: Floppy disk  
COMPUTER: IBM PC compatible  
OPERATING SYSTEM: PC-DOS/MS-DOS  
SOFTWARE: PatentIn Release #1.0, Version #1.25  
CURRENT APPLICATION DATA:  
APPLICATION NUMBER: US/08/845,998  
FILING DATE:  
CLASSIFICATION: 435  
ATTORNEY/AGENT INFORMATION:

NAME: Van Amsterdam, John R.  
 REGISTRATION NUMBER: 40,212  
 REFERENCE/DOCKET NUMBER: L0461/7008  
 TELECOMMUNICATION INFORMATION:  
 TELEPHONE: (617)720-3500  
 TELEFAX: (617)720-2441  
 INFORMATION FOR SEQ ID NO: 7:  
 SEQUENCE CHARACTERISTICS:  
 LENGTH: 4524 base pairs  
 TYPE: nucleic acid  
 STRANDEDNESS: double  
 TOPOLOGY: linear  
 MOLECULE TYPE: cDNA  
 HYPOTHEICAL: NO  
 ANTI-SENSE: NO  
 FEATURE:  
 NAME/KEY: CDS  
 LOCATION: 174..1433  
 US-08-845-998-7

Query Match  
 Best Local Similarity 5.9%; Score 44; DB 2; Length 4524;  
 Matches 180; Conservative 0; Mismatches 175; Indels 11; Gaps 2;  
 Db 21 TGAGCGGCGCAGCCGCGGAGATCTGAGACCATGAGGCGCGCGGAGCGCATCTG 80  
 556 TGCCCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 615  
 Oy 81 GATGCGCTGAGACCTGAGCCGCGGAGAGCTCAAGAGTTCAGAGTGAAGCTGCTG 140  
 Db 616 GGGGCGGTGGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGG 675  
 Oy 141 GTGCCGCTG--CGGAGGCGTACGAGGCGCATCCGCGGCGCGCGCTGTTCATGAGC 198  
 Db 676 GCGGTGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCT 735  
 Oy 199 CCTTGACCTACCGAGACCTGTGCTTACCTGAGAGCTTACGAGAGCTTACGAGAG 258  
 Db 736 GCGACCCCTACCGAGAGCTTACCTGAGAGCTTACGAGAGCTTACGAGAGCTTAC 258  
 Oy 259 CCGCTAACGTCGCGCGGAGATGAGGCTGCAAGAGATGAGGCGGAGCTGAGAGAG 318  
 Db 796 CCATGACATTCCTGCGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 846  
 Oy 319 CGCACAGAGGCTGAGAGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 846  
 Db 847 CGCACAGAGGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCGCG 906  
 379 AGCGAG 384  
 Db 907 CGGCGG 912

Search completed: December 13, 2002, 08:28:31  
 Job time : 275 secs







XX The invention discloses the isolated polypeptides, and encoding nucleic acids, of murine and human caspase recruitment domain (CARD)-5. Caspases (cysteineyl aspartate-specific proteinases) are central to the apoptotic program and responsible for the degradation of cellular proteins that lead to the morphological changes seen in cells undergoing apoptosis. CC Caspases interact with other caspases via their CARDS and different CC subtypes of CARDS may confer binding specificity. CARD-5 is an CC intracellular protein that is predicted to be involved in regulating CC caspase activation. CARD-5 activates the nuclear factor-kappa B CC (NF-kappaB) transcription factor pathway and binds the CARDS of CC caspase-1, CARD-7 and itself. CARD-5 can, therefore, modulate CARD-5 CC activity and NF-kappaB activation, regulate cell growth and cell death CC and be used in gene therapy. The CARD-5 polypeptides are useful for CC identifying compounds which bind to them and modulate their activity and CC for detecting the presence of CARD-5 in a sample. CARD-5 polypeptides, CC nucleic acids, antibodies and modulators of CARD-5 expression or activity CC can be used to treat immune disorders such as chronic inflammatory CC diseases and disorders, Hashimoto's thyroiditis, graft rejection, CC sarcoidosis, atopic conditions (such as asthma and allergy), glomerular CC nephritis, human immunodeficiency virus (HIV) and bacterial infections CC (including tuberculosis and lepromatous leprosy) and in screening and CC detection assays. Modulators of CARD-5 activity or expression are also CC useful for treating autoimmune disorders, such as systemic lupus CC erythematosus and arthritis, cell depletion, neurological disorders, CC such as Alzheimer's disease, Parkinson's disease and spinal muscular CC atrophy, haematologic diseases, such as myelodysplastic syndrome and CC aplastic anaemia, myocardial infarction and stroke. The sequence CC presented is the human caspase recruitment domain-5 (CARD-5) cDNA.

XX  
XX  
SQ Sequence 740 BP; 146 A; 238 C; 236 G; 120 T; 0 other;

Query Match 100.0%; Score 740; DB 24; Length 740;

Best Local Similarity 100.0%; Pred. No. 2e-147; Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 CGCGTCGCGCTGAGCGGGGTGAGCGCGGCGCGGGATCTCTGAGCCATGGGGC 60  
Db 1 CGCGTCGCGCTGAGCGGGGTGAGCGCGGCGCGGGATCTCTGAGCCATGGGGC 60  
QY 61 GCGCGCGCGAGCGGATCTGAGTCCGTGAGAACTGACCGCGGAGAGCTCAAGAGT 120  
Db 61 GCGCGCGCGAGCGGATCTGAGTCCGTGAGAACTGACCGCGGAGAGCTCAAGAGT 120  
QY 121 TCAAGCTGAAGCTGCTGTGCGTGGCGCGGAGGCTACGGGCGATCCCGGGGGCG 180  
Db 121 TCAAGCTGAAGCTGCTGTGCGTGGCGCGGAGGCTACGGGCGATCCCGGGGGCG 180  
QY 181 CGCTGCTGCATGAGACGCTTGACCTCAACGAAAGCTGTGACGTTTACTGTGAGA 240  
Db 181 CGCTGCTGCATGAGACGCTTGACCTCAACGAAAGCTGTGACGTTTACTGTGAGA 240  
QY 241 CCTAGCGCGCGAGCTACCGGCTAAGCTGTGCGCGACATGGGCTGAGAGATGGCG 300  
Db 241 CCTAGCGCGCGAGCTACCGGCTAAGCTGTGCGCGACATGGGCTGAGAGATGGCG 300  
QY 301 GCGAGCTGCGAGGGGCGGCGACGACGAGGCTGTGAGACCGCGGCACTGGGATCCAGGCC 360  
Db 301 GCGAGCTGCGAGGGGCGGCGACGACGAGGCTGTGAGACCGCGGCACTGGGATCCAGGCC 360  
QY 361 CTGCTAGTGGAGCGCAACGCGCTGACCTTTATAGACAGACCGGGCTGCGGTTA 420  
Db 361 CTGCTAGTGGAGCGCAACGCGCTGACCTTTATAGACAGACCGGGCTGCGGTTA 420  
QY 421 TCGCGAGGGCTACAAACGTTGAGTGGCTGTGATGCTGTGAAGAGTCTTGACGG 480  
Db 421 TCGCGAGGGCTACAAACGTTGAGTGGCTGTGATGCTGTGAAGAGTCTTGACGG 480  
QY 481 ATGAGAGTACGAGGAGTGGCGGCGAGCGGCGCAACCAACCAAGATGCGGAAGCTCT 540  
Db 481 ATGAGAGTACGAGGAGTGGCGGCGAGCGGCGCAACCAACCAAGATGCGGAAGCTCT 540  
QY 541 TCAGTTTCAACACGAGCTGGAAGCTGACCTGCAAGAGCTTGTCTTCAGAGCCCTAAGG 600

Db 541 TCAGTTTCAACACGAGCTGGAAGCTGACCTGCAAGAGCTTGTCTTCAGAGCCCTAAGG 600  
QY 601 AGTCCAGAGTCTTACCTGTGTGAGAGACTGAGGAGAGCTGAGGCTCTTCCAGCAAC 660  
Db 601 AGTCCAGAGTCTTACCTGTGTGAGAGACTGAGGAGAGCTGAGGCTCTTCCAGCAAC 660  
QY 661 TCGGTCAGCCCTGGGCAATCCCAACCAATCAATCTGATCTTTTATACCAAT 720  
Db 661 TCGGTCAGCCCTGGGCAATCCCAACCAATCAATCTGATCTTTTATACCAAT 720  
QY 721 ATAGCAAAAGCCAGCTTGAA 740  
Db 721 ATAGCAAAAGCCAGCTTGAA 740

RESULT 3  
ABK87967/c  
ID ABK87967 standard; DNA: 740 BP.

XX ABK87967;

DT 07-OCT-2002 (first entry)

XX Human caspase recruitment domain-5 (CARD-5) cDNA complementary strand.

XX Human: ss; caspase recruitment domain-5; CARD-5; antiinflammatory;

XX immunosuppressive; caspase; cysteineyl aspartate-specific proteinase;

XX apoptosis; nuclear factor-kappa B; NF-kappaB; transcription factor;

XX cell proliferation; gene therapy; immune disorder;

XX chronic inflammatory disease; Hashimoto's thyroiditis; graft rejection;

XX sarcoidosis; atopy; asthma; allergy; glomerular nephritis;

XX human immunodeficiency virus; HIV; bacterial infection; tuberculosis;

XX lepromatous leprosy; autoimmune disorder; systemic lupus erythematosus;

XX arthritis; cell depletion; neurological disorder; Alzheimer's disease;

XX Parkinson's disease; spinal muscular atrophy; haematologic disease;

XX myelodysplastic syndrome; aplastic anaemia; myocardial infarction;

XX stroke.

XX Homo sapiens.

XX MO200244354-A2.

XX 06-JUN-2002.

XX 29-NOV-2001; 2001WO-US44894.

XX 01-DEC-2000; 2000US-0728721.

XX 24-APR-2001; 2001US-0841879.

XX (MILL-) MILLENIUM PHARM INC.

XX Bertin J;

XX MPI; 2002-557538/59.

XX Novel isolated murine or human caspase recruitment domain (CARD)-5

XX polypeptide, useful for treating immune disorders such as Hashimoto's

XX thyroiditis, graft rejection, allergy, glomerular nephritis,

XX tuberculosis -

PS Claim 8; Fig 3; 100pp: English.

XX The invention discloses the isolated polypeptides, and encoding nucleic

XX acids, of murine and human caspase recruitment domain (CARD)-5. Caspases

XX (cysteineyl aspartate-specific proteinases) are central to the apoptotic

XX program and responsible for the degradation of cellular proteins that

XX lead to the morphological changes seen in cells undergoing apoptosis.

XX Caspases interact with other caspases via their CARDS and different

XX subtypes of CARDS may confer binding specificity. CARD-5 is an

XX intracellular protein that is predicted to be involved in regulating

XX caspase activation. CARD-5 activates the nuclear factor-kappa B

XX (NF-kappaB) transcription factor pathway and binds the CARDS of



Db 28 CGGCTGACGGGGGTGAGCGGCGGACGGCCGGGGATCCTGGAGCCATGGGGCGGCGC 87  
 QY 67 GCGAGCCCATCTCTGATGTTGGCTTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 126  
 Db 88 GCGAGCCCATCTCTGATGTTGGCTTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 147  
 QY 127 TGAAGCTGCTGTCGGGCTGCGGCTGCGGAGGGGCTACGGGGGATCCCGGGGGGGCGCTGC 186  
 Db 148 TGAAGCTGCTGTCGGGCTGCGGCTGCGGAGGGGCTACGGGGGATCCCGGGGGGGCGCTGC 207  
 QY 187 TGTTCATGAGCAGCTTGTGACCTCACCAGCAAGCTGTCTTACTCTGAGAACCTAG 246  
 Db 208 TGTTCATGAGCAGCTTGTGACCTCACCAGCAAGCTGTCTTACTCTGAGAACCTAG 267  
 QY 247 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCAGAGAGATGGCGGCGAC 306  
 Db 268 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCAGAGAGATGGCGGCGAC 327  
 QY 307 TCGAGCGGCGCAGCGACGAGGGGCTGAGAGCGGCGGACCTGGGATCCAGGGCCCTCC 366  
 b 328 TCGAGCGGCGCAGCGACGAGGGGCTGAGAGCGGCGGACCTGGGATCCAGGGCCCTCC 387  
 QY 367 AGTCGCGACGCAAGCCAGGCTGTCACTTTATAGCCAGCAGCGGCTGCGCTTATCGCA 426  
 Db 388 AGTCGCGACGCAAGCCAGGCTGTCACTTTATAGCCAGCAGCGGCTGCGCTTATCGCA 447  
 QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTGACGGGAAGTCTTGACGGATGAGC 486  
 Db 448 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTGACGGGAAGTCTTGACGGATGAGC 507  
 QY 487 AGTACCAGCAGTGGCGGCGGAGCCGACCAACCAAGAGGGAAGGCTTTCAGTT 546  
 Db 508 AGTACCAGCAGTGGCGGCGGAGCCGACCAACCAAGAGGGAAGGCTTTCAGTT 567  
 QY 547 TCACACACGCTTGGAACTGGAACTGGAACTGGCTTCTCCAGGCCCTTAAGGAGATGCC 606  
 Db 568 TCACACACGCTTGGAACTGGAACTGGAACTGGCTTCTCCAGGCCCTTAAGGAGATGCC 627  
 QY 607 AGTCCACTGCTGTGGAGGAGCTGGAGCGGAGCTGAGGCTCTTCCAGCAAACTCCGGT 666  
 Db 628 AGTCCACTGCTGTGGAGGAGCTGGAGCGGAGCTGAGGCTCTTCCAGCAAACTCCGGT 687  
 QY 667 CAGCCCTGGCAATCCCAACAATCATCTGAAATGATCTTTTATACAAATATACGA 726  
 Db 688 CAGCCCTGGCAATCCCAACAATCATCTGAAATGATCTTTTATACAAATATACGA 747  
 QY 727 AAAGCCAGCTGAA 740  
 Db 748 AAAGCCAGCTGAA 761  
 RESULT 5  
 AAL47126  
 ID AAL47126 standard; DNA; 782 BP.  
 AC AAL47126;  
 XX 20-AUG-2002 (first entry)  
 DE Pyrin domain containing protein Pycard coding sequence.  
 XX Pyrin domain; PYD domain; antiinflammatory; antiapoptosis;  
 KW antiarteriosclerotic; antiproliferative; antibacterial; virucide;  
 KW neuroprotective; antiarthritic; antineoplastic; antiasthmatic;  
 KW nephrotoxic; osteoporotic; neurotoxic; intracellular signal transduction;  
 KW inflammation; Alzheimer's disease; infection; psoriasis; asthma;  
 KW arteriosclerosis; multiple sclerosis; rheumatoid arthritis; sarcoidosis;  
 XX osteoarthritis; glomerulonephritis; gene; ds.  
 OS Unidentified.  
 XX  
 XX  
 XX WO200240668-A2.  
 PN

PD 23-MAY-2002.  
 XX  
 XX 30-OCT-2001: 2001WO-EP12545.  
 XX  
 PR 15-NOV-2000: 2000DE-1056687.  
 PR 30-NOV-2000: 2000DE-1059595.  
 XX  
 XX (APOT-) APOTEC RES & DEV LTD.  
 PA  
 PI Tschopp J, Martinon F;  
 PI  
 DR MPI: 2002-427093/45.  
 DR P-PSDB; AAO17854.  
 XX  
 XX New DNA encoding protein with pyrin domain, useful for treating  
 PT diseases involving impaired signal transduction, particularly  
 PT inflammation, also proteins and antibodies  
 XX  
 PS Claim 5; Fig 1; 116pp; German.  
 XX  
 CC The present invention relates the DNA and their encoded proteins, where  
 CC the proteins contain at least one PYD (pyrin) domain. These can be used  
 CC to treat diseases associated with impaired intracellular signal  
 CC transduction, particularly inflammation such as psoriasis,  
 CC arteriosclerosis, bacterial or viral infections (particularly meningitis  
 CC and pneumonia), multiple sclerosis, rheumatoid arthritis, asthma,  
 CC sarcoidosis, glomerulonephritis and osteoarthritis, and also Alzheimer's  
 CC and Parkinson's diseases. The present sequence is a coding sequence of  
 the invention.  
 XX  
 XX  
 SO Sequence 782 BP; 158 A; 251 C; 246 G; 127 T; 0 other;  
 Query Match 99.2%; Score 734; DB 24; Length 782;  
 Best Local Similarity 100.0%; Pred. No. 3.7e-146;  
 Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 QY 7 CCGCTGACGGGGGTGAGGGGCGGAGCGGCGGAGTCTGGAGCCATGGGGCGGCGC 66  
 Db 40 CCGCTGACGGGGGTGAGGGGCGGAGCGGCGGAGTCTGGAGCCATGGGGCGGCGC 99  
 QY 67 GCGAGCCCATCTCTGATGTTGGCTTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 126  
 Db 100 GCGAGCCCATCTCTGATGTTGGCTTGGAGAACCTGACCCCGAGAGGCTCAAGATTAAAG 159  
 QY 127 TGAAGCTGCTGTCGGGCTGCGGCTGCGGAGGGGCTACGGGGGATCCCGGGGGGGCGCTGC 186  
 Db 160 TGAAGCTGCTGTCGGGCTGCGGCTGCGGAGGGGCTACGGGGGATCCCGGGGGGGCGCTGC 219  
 QY 187 TGTTCATGAGCAGCTTGTGACCTCACCAGCAAGCTGTCTTACTCTGAGAACCTAG 246  
 Db 220 TGTTCATGAGCAGCTTGTGACCTCACCAGCAAGCTGTCTTACTCTGAGAACCTAG 279  
 QY 247 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCAGAGATGGCGGCGAC 306  
 Db 280 GCGCCGAGCTCACCGCTTAACCTGCTGCGGACATGGGCTGCAGAGATGGCGGCGAC 339  
 QY 307 TCGAGCGGCGCAGCGACGAGGGGCTGAGAGCGGCGGACCTGGGATCCAGGGCCCTCC 366  
 Db 340 TCGAGCGGCGCAGCGACGAGGGGCTGAGAGCGGCGGACCTGGGATCCAGGGCCCTCC 399  
 QY 367 AGTCGCGACGCAAGCCAGGCTGTCACTTTATAGCCAGCAGCGGCTGCGCTTATCGCA 426  
 Db 400 AGTCGCGACGCAAGCCAGGCTGTCACTTTATAGCCAGCAGCGGCTGCGCTTATCGCA 459  
 QY 427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTGACGGGAAGTCTTGACGGATGAGC 486  
 Db 460 GGGTCACAAACGTTGAGTGGCTGCTGATGCTGTGACGGGAAGTCTTGACGGATGAGC 519  
 QY 487 AGTACCAGCAGTGGCGGCGGAGCCGACCAACCAAGAGGGAAGGCTTTCAGTT 546  
 Db 520 AGTACCAGCAGTGGCGGCGGAGCCGACCAACCAAGAGGGAAGGCTTTCAGTT 579  
 QY 547 TCACACACGCTTGGAACTGGAACTGGAACTGGCTTCTCCAGGCCCTTAAGGAGATGCC 606



|||||  
Db 602 GTCCTACCTGCTGAGAGACTGGAGCGGAGCTGAGGCTCTCTCCAGCAACACTCGGCTC 661  
QY 668 AGCCCTGCGCAATCCACCAATATCTGATCTGATCTTTTATACATATATACGAA 727  
|||||  
Db 662 AGCCCTGCGCAATCCACCAATATCTGATCTGATCTTTTATACATATATACGAA 721  
QY 728 AGCCAGCTTGAA 740  
|||||  
Db 722 AGCCAGCTTGAA 734

RESULT 7  
AA233631

ID AA233631 standard; cDNA; 779 BP.

AA233631;

08-DEC-1999 (first entry)

Human breast tumour-associated EST 21.

Expressed sequence tag; EST; human; breast; cancer; gene therapy;  
treatment; tumour; cytostatic; medication; ss.

Homo sapiens.

DE19813839-A1.

23-SEP-1999.

20-MAR-1998; 98DE-1013839.

20-MAR-1998; 98DE-1013839.

(META-) METAGEN GES GENOMFORSCHUNG MBH.

Specht T, Hinzmann B, Schmitt A, Pilarsky C, Dahl E, Rosenthal A;

WPI; 1999-528981/45.

Human nucleic acid sequences and protein products from tumor breast  
tissue, useful for breast cancer therapy -

Claim 1a; 101; 188pp; German.

This invention describes novel human nucleic acid sequences from tumor  
breast tissue which have cytostatic activity. The nucleic acid sequences  
can be used to produce and isolate full-length gene sequences. They can  
be used to express proteins, which can be used as tools to find an  
activity against breast cancer. The sequences can be used in sense or  
antisense form. They are especially useful for medicaments for gene  
therapy to treat breast cancer. AA233611-248617 represents expressed  
sequence tags described in the method of the invention.

SQ Sequence 779 BP; 149 A; 252 C; 251 G; 127 T; 0 other;

Query Match 99.1%; Score 733; DB 20; Length 779;  
Best Local Similarity 100.0%; Pred. No. 6e-146;  
Matches 733; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 7 CGGCTGACAGCGGGGAGCGGCGAGCGCGGGGATCCTGGAGCATGGGCGGCGC 66  
|||||  
Db 47 CGGCTGACAGCGGGGAGCGGCGGCGAGCGCGGGGATCCTGGAGCATGGGCGGCGC 106  
|||||  
QY 67 GCGAGCCCATCTGATGCGCTGAGAGACCTGACCGCGAGAGAGCTCAAGATTCAAGC 126  
|||||  
Db 107 GCGAGCCCATCTGATGCGCTGAGAGACCTGACCGCGAGAGAGCTCAAGATTCAAGC 166  
|||||  
QY 127 TGAAGTGTCTGCTGCGGCTGCGGAGGAGGCTACGGGCGCATCCGGGCGGCGCTGC 186  
|||||  
Db 167 TGAAGTGTCTGCTGCGGCTGCGGAGGAGGCTACGGGCGCATCCGGGCGGCGCTGC 226  
|||||

QY 187 TGTCCATGAGCGCTTGTGACCTTCACGACAGCTGCTAGCTTCTACCTGAGACTACG 246  
|||||  
Db 227 TGTCCATGAGCGCTTGTGACCTTCACGACAGCTGCTAGCTTCTACCTGAGACTACG 286  
|||||  
QY 247 GCGCCGAGCTCAACCGCTTAACGCTGCTGCGGAGATGGGCTGAGAGATGGCGGCGACG 306  
|||||  
Db 287 GCGCCGAGCTCAACCGCTTAACGCTGCTGCGGAGATGGGCTGAGAGATGGCGGCGACG 346  
|||||  
QY 307 TGCAGCGCGGCACGACGACGAGGCGCTGAGAGCGCGGCGACCTGGAGATCCAGGCCCTCTC 366  
|||||  
Db 347 TGCAGCGCGGCACGACGACGAGGCGCTGAGAGCGCGGCGACCTGGAGATCCAGGCCCTCTC 406  
|||||  
QY 367 AGTCGACGACCAAGCGAGCTGCACTTATAGACGACGCGGCTGAGCTTATGCGCA 426  
|||||  
Db 407 AGTCGACGACCAAGCGAGCTGCACTTATAGACGACGCGGCTGAGCTTATGCGCA 466  
|||||  
QY 427 GGGTCACAAAGCTTGAAGTGGCTGCTGAGATGCTGTAGCGGAAGGCTCTGACGAGATGAGC 486  
|||||  
Db 467 GGGTCACAAAGCTTGAAGTGGCTGCTGAGATGCTGTAGCGGAAGGCTCTGACGAGATGAGC 526  
|||||  
QY 487 AGTACGAGGCACTGGCGGCGGAGCCGACCAACCAAGCAAGATGCGGAAGCTTCACTT 546  
|||||  
Db 527 AGTACGAGGCACTGGCGGCGGAGCCGACCAACCAAGCAAGATGCGGAAGCTTCACTT 586  
|||||  
QY 547 TCACACGACGCTGGAAGCTGGAAGCTGGAAGCTGCTCCAGGCGCTTAAGGAGTCC 606  
|||||  
Db 587 TCACACGACGCTGGAAGCTGGAAGCTGGAAGCTGCTCCAGGCGCTTAAGGAGTCC 646  
|||||  
QY 607 AGTCTACCTGTGTGAGAGACCTGAGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGT 666  
|||||  
Db 647 AGTCTACCTGTGTGAGAGACCTGAGAGCGGAGCTGAGGCTCTTCCAGCAACACTCCGT 706  
|||||  
QY 667 CAGCCCTGCGCAATCCGACCAATCATCTGATCTGATCTTTTATACATATATACGA 726  
|||||  
Db 707 CAGCCCTGCGCAATCCGACCAATCATCTGATCTGATCTTTTATACATATATACGA 766  
|||||  
QY 727 AAAGCCAGCTTGA 739  
|||||  
Db 767 AAAGCCAGCTTGA 779  
|||||

RESULT 8  
AAH34052

ID AAH34052 standard; cDNA; 806 BP.

AAH34052;

03-SEP-2001 (first entry)

Human colon cancer antigen encoding cDNA SEQ ID NO:1134.

Human; colon cancer; colon cancer antigen; diagnosis; detection;  
colorectal carcinoma; ss.

Homo sapiens.

WO200122920-A2.

05-APR-2001.

28-SEP-2000; 2000WO-US26524.

29-SEP-1999; 99US-0157137.

03-NOV-1999; 99US-0163280.

(HUMA-) HUMAN GENOME SCI INC.

Ruben SM, Barash SC, Birse CE, Rosen CA;

WPI; 2001-235357/24.

P-PSDB; AAG74647.

Nucleic acids encoding 4277 human colon cancer-associated polypeptides,







CC the present invention.

XX \* Sequence 811 BP; 170 A; 253 C; 259 G; 128 T; 1 other;

Query Match 94.3%; Score 697.6; DB 21; Length 811;  
 Best Local Similarity 99.5%; Pred. No. 1.9e-138;  
 Matches 730; Conservative 1; Mismatches 0; Indels 3; Gaps 3;

OY 7 CGGCTGCAGCGGGGTGACGGGGGCGGAGGGGATCTTGAGACCATGGGGCGCGGC 66  
 |||||||  
 DB 68 CGGCTGCAGCGGGGTGACGGGGGCGGAGGGGATCTTGAGACCATGGGGCGCGGC 127  
 OY 67 GCGAGCCATCTTGATGCGGTGAGAACTGACCGCGAGAGCTCAAGAATTCAAGC 126  
 |||||||  
 DB 128 GCGAGCCATCTTGATGCGGTGAGAACTGACCGCGAGAGCTCAAGAATTCAAGC 187  
 OY 127 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGGATCCGGGGGCGCGTCG 186  
 |||||||  
 DB 188 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGGATCCGGGGGCGCGTCG 247  
 OY 187 TGTCCATGGAGCCCTTGACCTGACGAGCAACCTGTGACCTTCTACCTGGAGACTAG 246  
 |||||||  
 DB 248 TGTCCATGGAGCCCTTGACCTGACGAGCAACCTGTGACCTTCTACCTGGAGACTAG 307  
 OY 247 GCGCCGAGCTCACCGCTAAAGTGTGCGGAGACATGGGCTGCGAGAGATGGCGGGCAGC 306  
 |||||||  
 DB 308 GCGCCGAGCTCACCGCTAAAGTGTGCGGAGACATGGGCTGCGAGAGATGGCGGGCAGC 367  
 OY 307 TGCAGCGGGCCAGCAGCAGGAGGCTGTGAGAGCCGCGCAAGCTGGAGTCCAGGCCCTCTC 366  
 |||||||  
 DB 368 TGCAGCGGGCCAGCAGCAGGAGGCTGTGAGAGCCGCGCAAGCTGGAGTCCAGGCCCTCTC 427  
 OY 367 AGTCGGAGCCCAAGCCAGGAGCTGTGATGACCAAGCAGCAGCGGCTGCTTATCGCA 426  
 |||||||  
 DB 428 AGTCGGAGCCCAAGCCAGGAGCTGTGATGACCAAGCAGCAGCGGCTGCTTATCGCA 487  
 OY 427 GGGTACAAAGCTGTAGTGGCTGTGATGCTCTGTAGGGGAAGGTCCTGAGCGATGAGC 486  
 |||||||  
 DB 488 GGGTACAAAGCTGTAGTGGCTGTGATGCTCTGTAGGGGAAGGTCCTGAGCGATGAGC 547  
 OY 487 AGTACAGGAGCACTGGGGGCGGAGCCCAACCAAGCAAGATGGGGAAGCTCTTCAATT 546  
 |||||||  
 DB 548 AGTACAGGAGCACTGGGGGCGGAGCCCAACCAAGCAAGATGGGGAAGCTCTTCAATT 606  
 OY 547 TCCACACAGCCCTGAGACCTGAGACTGCAAGAGACTTCTCTCCAGGCCCTTAAGGAGTCCC 606  
 |||||||  
 DB 607 TCCACACAGCCCTGAGACCTGAGACTGCAAGAGACTTCTCTCCAGGCCCTTAAGGAGTCCC 666  
 OY 607 AGTCTTACCTGGTGGAGAGCTGAGAGGAGCTGAGGGCTCTCCAGCAACATCCGGT 666  
 |||||||  
 DB 667 AGTCTTACCTGGTGGAGAGCTGAGAGGAGCTGAGGGCTCTCCAGCAACATCCGGT 725  
 OY 667 CAGCCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACAAATATACGA 726  
 |||||||  
 DB 726 CA-SCCTGGCAATCCCAACAATCATCTGATCTGATCTTTTATACAAATATACGA 784  
 OY 727 AAAGCCAGCTTGA 740  
 |||||||  
 DB 785 AAAGCCAGCTTGA 798

RESULT 10

AAD03906 standard; cDNA: 713 BP.

AAD03906;

02-JUL-2001 (first entry)

Alternatively spliced form of human TMS1 cDNA (lacking exon2).

XX Human: target of methylation-induced silencing-1; TMS1: cytostatic;  
 XX antiproliferative; apoptosis inducer; gene therapy; CpG island;  
 KW

KW caspase-recruiting domain; CARD; cancer; breast; ss.  
 XX Homo sapiens.  
 OS  
 XX Key Location/Qualifiers  
 FH CDS 75..605  
 FT /tag= a  
 FT /product= "Alternatively spliced form of human TMS1  
 FT protein lacking exon2"  
 FT  
 PN W0200129235-A2.  
 XX  
 PD 26-APR-2001.  
 XX  
 PP 18-OCT-2000; 2000WO-US28747.  
 XX  
 PR 18-OCT-1999; 99US-0159975.  
 XX  
 PA (UYEM-) UNIV EMORY.  
 XX  
 PI Vertino PM.  
 XX  
 DR WPI; 2001-290922/30.  
 DR P-PSDB; AAE00594.  
 XX  
 PT Novel gene TMS1, transcriptionally silenced due to increased  
 PT methylation useful for identifying subject at risk of developing tumor  
 PT characterized by abnormal methylation, for treating cancer by inducing  
 PT apoptosis  
 PT  
 PS  
 XX  
 XX Claim 68; Page 122; 124pp; English.  
 XX  
 CC The invention relates to identification of target of methylation-induced  
 CC silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to  
 CC abnormal methylation of a CpG island in its 5' regulatory region. TMS1  
 CC consists of a carboxy terminal caspase-recruiting domain (CARD) and  
 CC plays a role in induction of apoptosis. TMS1 gene and protein are useful  
 CC as tools for diagnosing and treating a subject at risk of developing  
 CC cancer (e.g. breast cancer) characterized by abnormal CpG methylation or  
 CC abnormally low levels of TMS1 expression products. Unique fragments of  
 CC TMS1 gene are used as probes. TMS1 gene is useful in gene therapy.  
 CC TMS1 molecule is also useful for treating abnormal cell proliferation by  
 CC increasing TMS1 polypeptide level to an above normal level. The CpG  
 CC island region of TMS1 or its fragments are used to study the methylation  
 CC patterns apart from any coding region contained in it.  
 CC The present sequence is alternatively spliced form of human target of  
 CC methylation-induced silencing-1 (TMS1) cDNA lacking exon2.  
 CC  
 SQ Sequence 713 BP; 148 A; 224 C; 223 G; 118 T; 0 other;  
 Query Match 82.4%; Score 610; DB 22; Length 713;  
 Best Local Similarity 92.2%; Pred. No. 6.1e-120;  
 Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

OY 7 CGGCTGCAGCGGGGTGACGGGGGCGGAGGGGATCTTGAGACCATGGGGCGCGGC 66  
 |||||||  
 DB 28 CGGCTGCAGCGGGGTGACGGGGGCGGAGGGGATCTTGAGACCATGGGGCGCGGC 87  
 OY 67 GCGAGCCATCTTGATGCGGTGAGAACTGACCGCGAGAGCTCAAGAATTCAAGC 126  
 |||||||  
 DB 88 GCGAGCCATCTTGATGCGGTGAGAACTGACCGCGAGAGCTCAAGAATTCAAGC 147  
 OY 127 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGGATCCGGGGGCGCGTCG 186  
 |||||||  
 DB 148 TGAAGCTCTGTGGTGGCTGCGCGAGGGGCTACGGGGGATCCGGGGGCGCGTCG 207  
 OY 187 TGTCCATGGAGCCCTTGACCTGACGAGCAACCTGTGACCTTCTACCTGGAGACTAG 246  
 |||||||  
 DB 208 TGTCCATGGAGCCCTTGACCTGACGAGCAACCTGTGACCTTCTACCTGGAGACTAG 267  
 OY 247 GCGCCGAGCTCACCGCTAAAGTGTGCGGAGACATGGGCTGCGAGAGATGGCGGGCAGC 306  
 |||||||  
 DB 268 GCGCCGAGCTCACCGCTAAAGTGTGCGGAGACATGGGCTGCGAGAGATGGCGGGCAGC 327

OY 307 TCGAGCGGCGCACGACGAGGCTCTGAGCCGCGCAGCTGGATCCAGGCCCTCTCTC 366  
 Db 328 TCGAGCGGCGCACGACGAGGCTCTGAGCCGCGCAGCTGGATCCAGGCCCTCTCTC 347  
 OY 367 AGTCGGACGACCAAGCGCCCTGACCTTTATAGACAGACCGGCTCTCTCTCTCTC 426  
 Db 348 -----GGCTGACCTTTATAGACAGACCGGCTCTCTCTCTCTCTCTCTCTC 390  
 OY 427 GGCTCACAACAGCTTGAAGTGTCTCTGATGCTCTGAGGAGGAGTCTCTACGATGAGC 486  
 Db 391 GGCTCACAACAGCTTGAAGTGTCTCTGATGCTCTGAGGAGGAGTCTCTACGATGAGC 450  
 OY 487 AGTACGACGACGTCGGGCGGAGCCGACCCACCAACCAAGCAAGATGCGGAAGCTCTTCA 546  
 Db 451 AGTACGACGACGTCGGGCGGAGCCGACCCACCAACCAAGCAAGATGCGGAAGCTCTTCA 510  
 OY 547 TCACACGACGCTGGAACCTGACCTGACGAGCTTGTCTCTCCAGGCGCTTAAGGAGTCC 606  
 Db 511 TCACACGACGCTGGAACCTGACCTGACGAGCTTGTCTCTCCAGGCGCTTAAGGAGTCC 570  
 OY 607 AGTCTACCTGTGTGAGGAGCTGTGAGCGAGCTGAGGCTCTCTCCAGCAACACTCCGGT 666  
 Db 571 AGTCTACCTGTGTGAGGAGCTGTGAGCGAGCTGAGGCTCTCTCCAGCAACACTCCGGT 630  
 OY 667 CAGCCCTGCAATCCCAACCAATCTCTGATCTGATCTTTTATACAAATATAGCA 726  
 Db 631 CAGCCCTGCAATCCCAACCAATCTCTGATCTGATCTTTTATACAAATATAGCA 690  
 OY 727 AAGCCAGCTTGAA 740  
 Db 691 AAGCCAGCTTGAA 704  
  
 RESULT 11  
 AAH34053  
 ID AAH34053 standard: cDNA; 639 bp.  
 AC AAH34053;  
 AC 03-SEP-2001 (first entry)  
 DE Human colon cancer antigen encoding cDNA SFO ID NO:1135.  
 DE Human; colon cancer; colon cancer antigen; diagnosis; detection;  
 KM colorectal carcinoma; ss.  
 XX Homo sapiens.  
 XX WO200122920-A2.  
 XX 05-APR-2001.  
 XX 28-SEP-2000; 2000WO-US26524.  
 XX 29-SEP-1999; 99US-0157137.  
 XX 03-NOV-1999; 99US-0163280.  
 XX (HUMA-) HDMA GENOME SCI INC.  
 XX Ruben SM, Barash SC, Birse CE, Rosen CA;  
 XX WPI; 2001-235357/24.  
 XX P-PSDB; AAG74648.  
 XX Nucleic acids encoding 4277 human colon cancer-associated polypeptides,  
 XX useful for preventing, diagnosing and/or treating colorectal cancers -  
 XX Claim 1; Page 2955; 9803pp; English.  
 XX AAH32943 to AAH37195 and AAG73514 to AAG77788 represent human colon  
 XX cancer-associated nucleic acid molecules (N) and proteins (P), where  
 XX the proteins are collectively known as colon cancer antigens. The colon

CC Cancer antigens have cytosolic activity and can be used in gene  
 CC therapy and vaccine production. N and P may be used in the prevention,  
 CC diagnosis and treatment of diseases associated with inappropriate P  
 CC expression. For example, N and P may be used to treat disorders  
 CC associated with decreased expression by rectifying mutations or deletions  
 CC in a patient's genome that affect the activity of P by expressing of P.  
 CC Additionally, N may be used to supplement the patient's own production of P,  
 CC by inserting the nucleic acids into a host cell and culturing the cell  
 CC to express the proteins. N and P can be used in the prevention, diagnosis  
 CC and treatment of colorectal carcinomas and cancers. AAH37195 to AAH37204  
 CC present invention. 682 and page 7053 of the sequence listing were  
 CC N.B. Pages 666 to 682 and page 7053 of the sequence listing were  
 CC missing at time of publication, meaning no sequences are present for  
 CC SFO ID NO:1027 to 1052, 7921 and 7922.  
 XX  
 SO Sequence 639 bp; 146 A; 198 C; 189 G; 106 T; 0 other;  
  
 Query Match 71.88; Score 531; DB 22; Length 639;  
 Best Local Similarity 94.98; Pred. No. 36-103;  
 Matches 595; Conservative 0; Mismatches 20; Indels 12; Gaps 4;  
  
 OY 124 AGCTGAAGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 176  
 Db 2 AGCTGAAGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 176  
 OY 177 GAGCGGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 176  
 Db 62 GATGCGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 121  
 OY 234 CTGGAAGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 293  
 Db 122 CTGGAAGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 181  
 OY 294 ATGCGCGGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 353  
 Db 182 ATGCGCGGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 241  
 OY 354 CAGGCGGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 413  
 Db 242 CAGGCGGCTGTGTCATGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 301  
 OY 414 GCGCTTATGCGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 473  
 Db 302 GCGCTTATGCGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG-----G 361  
 OY 474 CTGAGGATGAGCTAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 533  
 Db 362 CTGAGGATGAGCTAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 420  
 OY 534 AAGCTTTCAGTTTACACACAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 593  
 Db 421 AAGCTTTCAGTTTACACACAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 480  
 OY 594 CTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 653  
 Db 481 CTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 540  
 OY 654 GCAACACTCCGCTGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 713  
 Db 541 GCAACACTCCGCTGAGGCTGTGAGGAGGCTGTGAGGAGGCTAGCGGCGATCCCGG 599  
 OY 714 ACACAATATAGCAAAAGCCAGCTGAA 740  
 Db 600 ACACAATATAGCAAAAGCCAGCTGAA 626  
  
 RESULT 12  
 AAC98638  
 ID AAC98638 standard: cDNA; 432 bp.  
 AC AAC98638;

XX	09-MAR-2001	(first entry)	
DT			
DE	Human colon cancer antigen nucleotide sequence SEQ ID NO:648.		
XX			
XX	Human; colon cancer; colon cancer antigen; diagnosis; detection;		
KW	identification; cytostatic; cardioactive; neuroprotective; vulnerary;		
KW	immunomodulatory; muscular; gynaecological; gastrointestinal;		
KW	neurotropic; antiinfective; antibacterial; gene therapy; wound;		
KW	neural disorder; immune system disorder; muscular disorder;		
KW	reproductive disorder; gastrointestinal disorder; renal disorder;		
KW	infectious disease; cardiovascular disorder; ss.		
XX			
XX	Homo sapiens.		
XX			
PN	WO200055351-A1.		
XX			
PD	21-SEP-2000.		
XX			
PF	08-MAR-2000; 2000WO-US05883.		
PR	12-MAR-1999; 99US-0124270.		
XX			
PA	(HUMA-) HUMAN GENOME SCI INC.		
XX			
PI	Rosen CA, Ruben SM;		
DR	WPI: 2000-587534/55.		
DR	P-PSDB; AAB53881.		
XX			
PT	Colon cancer associated gene sequences, referred to as colon cancer		
XX	antigens, useful for the treatment, prevention, and diagnosis of colon		
PT	disorders such as colon cancer -		
PS			
XX	Claim 1; Page 1175; 2104pp: English.		
CC	AAC97991 to AAC98763 encode the human colon cancer associated proteins,		
CC	called human colon cancer antigens, given in AAB53234 to AAB54006. The		
CC	human colon cancer antigens can have cytostatic, cardioactive, muscular;		
CC	neuroprotective, immunomodulatory, gynaecological, gastrointestinal,		
CC	vulnerary, nephrotropic, antiinfective and antibacterial activities, and		
CC	can be used in gene therapy. The colon cancer antigen polynucleotides,		
CC	proteins and antibodies to the proteins are useful for the prevention,		
CC	treatment and diagnosis of colon disorders, such as colon cancer. The		
CC	polynucleotides may be used in diagnostics and research, such as for		
CC	chromosome identification, and as hybridisation probes. The proteins		
CC	may also be used to prevent diseases such as neural disorders, immune		
CC	system disorders, muscular disorders, reproductive disorders, immune		
CC	gastrointestinal disorders, wounds, renal disorders, infectious		
CC	diseases, and cardiovascular disorders. AAC98764 to AAC98772 and		
CC	AAB54007 represent sequences used in the exemplification of the present		
CC	invention.		
XX			
SO	Sequence 432 BP; 77 A; 142 C; 152 G; 61 T; 0 other;		
XX			
Query Match	52.0%; Score 384.6; DB 21; Length 432;		
Best Local Similarity	98.4%; Pred. No. 2.6e-72;		
Matches 420; Conservative	0; Mismatches 4; Indels 3; Gaps 3;		
QY	9 GCTGACGGGGGTAGAGCGGGGACCGGCGGGGATCTCGAAGCATGGGGCGCGCGC 68		
DB	8 GCTGACGGGGGTAGAGCGGGGACCGGCGGGGATCTCGAAGCATGGGGCGCGCGC 67		
QY	69 GACGCACTCTGGATGAGCTGGAGAACTGACCGCGGAGGAGCTCAAGAGTTCAAGG 128		
DB	68 GACGCACTCTGGATGAGCTGGAGAACTGACCGCGGAGGAGCTCAAGAGTTCAAGG 127		
QY	129 AAGCTGCTGTGCTGCGCTGCGCGGAGGCTACGGGCGCATCCCGCGGGCGCGCTGCTG 188		
DB	128 AAGCTGCTGTGCTGCGCTGCGCGGAGGCTACGGGCGCATCCCGCGGGCGCGCTGCTG 187		
QY	189 TCCATGAGCGCTTGAGACTCACGCAAGCTGGTTCAGCTTCTACCTGGAGACCTAAGGC 248		

Db	188	TCGATGAGCGGCTTGAGACCTCAGCAGACAGCGTGGTCAGCTTCACTACCTGGAGACCTACGGC	247		
Qy	249	GCCGAGCTCACCGCTAACGTGCTCGCGCAGACATGGGCGCTCGACGAGAGATGGCCGGGACGCTG	308		
Db	248	GCCGAGCTCACCGCTAACGTGCTCGCGCAGACATGGGCGCTCGACGAGAGATGGCCGGGACGCTG	307		
Qy	309	CAGGCGGCACGACACAGGCGCTCGGAGCCGCGCAGCTGGGATCCAGGCGCCCTCCACG	368		
Db	308	CAGGCGGCACGACACAGGCGCTCGGAGCCGCGCA-CTGGGATCCAGGCGCCCTCCACG	366		
Qy	369	TCGGCAGCCCAAGCCAGGCGCTGACTTT-ATAGACACAGACCGGGGCTGCGTTATCGCGAG	427		
Db	367	TCGGCAGCCCAAGCCAGGCGCTGACTTTATATAGACACAGCAGCGGCTTCG-TTATCGCGAA	425		
Qy	428	GGTCACA 434			
Db	426	GGTCMAA 432			
RESULT 13					
ID	AAD03907	AAD03907 standard; cDNA; 405 BP.			
XX	AAD03907;				
DT	02-JUL-2001	(first entry)			
DE	Alternatively spliced form of human TMS1 cDNA (lacking exon3).				
KM	Human; target of methylation-induced silencing-1; TMS1; cytostatic;				
KW	antiproliferative; apoptosis inducer; gene therapy; Cpg Island;				
KM	caspase-recruiting domain; CARD; cancer; breast; ss.				
OS	Homo sapiens.				
EH	key	Location/Qualifiers			
FT	CDS	75..404			
FT		/*tag a			
FT		/product= "Alternatively spliced form of human TMS1			
FT		protein lacking exon3"			
FT		/note= "CDS does not include stop codon"			
FT		/partial			
XX	WO200129235-A2.				
XX	26-APR-2001.				
PD					
XX	18-OCT-2000; 2000WO-US28747.				
PF					
XX	18-OCT-1999; 99US-0159975.				
PR					
XX	(UYEM-) UNIV EMORY.				
PA					
XX	Vertlino PM;				
PI					
XX	WPI; 2001-290922/30.				
DR					
XX	P-PSDB; AAE00595.				
XX					
PT	Novel gene TMS1, transcriptionally silenced due to increased				
PT	methylation useful for identifying subject at risk of developing tumor				
PT	characterized by abnormal methylation, for treating cancer by inducing				
PT	apoptosis				
XX					
PS	Claim 106; Page 123-124; 12App; English.				



QY	621	GAGGACCTGGAGCGGACTGAGGCTCCTTCCAGCAACACTCCGTCAGCCCTGGCAAT	680
Dd	2341	GAGGACCTGGAGCGGACTGAGGCTCCTTCCAGCAACACTCCGTCAGCCCTGGCAAT	2400
QY	681	CCCACCAATCATCTGATGTATCTTTTATATACACAATATACGAAGAACCAGCTTGAA	740
Dd	2401	CCCACCAATCATCTGATGTATCTTTTATATACACAATATACGAAGAACCAGCTTGAA	2460
<b>RESULT 15</b>			
ID	AAD03894	standard; DNA: 356 BP.	
XX	AAD03894;		
DT	02-JUL-2001	(first entry)	
De		Human target of methylation-induced silencing-1 (TMS1) exon3 DNA.	
XN		Human: target of methylation-induced silencing-1; TMS1; cytostatic;	
KM		antiproliferative; apoptosis inducer; gene therapy; Cpg Island;	
KW		caspase-recruiting domain; CARD; cancer; breast; ds.	
XS		Homo sapiens.	
OS			
FH	Key	Location/Qualifiers	
FT	CDS	3..257	
FT		/tag= a	
FT		/product= "Human TMS1 exon3 protein"	
FT		/note= "CDS does not include start codon"	
FT		/partial	
XX			
PN	WO200129235-A2.		
PD	26-APR-2001.		
PF	18-OCT-2000; 2000MO-US28747.		
PR	18-OCT-1999; 99US-0159975.		
PA	(UYEM-) UNIV EMORY.		
PI	Vertino PM;		
DR	WPI; 2001-290922/30.		
DR	P-PADB; AAE00591.		
XX			
XX			
PT			
PS			
XX			
XX			
CC	Claim 68; Page 116-117; 124pp; English.		
CC	The invention relates to identification of target of methylation-induced		
CC	silencing-1 (TMS1) gene. This gene is transcriptionally silenced due to		
CC	abnormal methylation of a CpG island in its 5' regulatory region. TMS1		
CC	consists of a carboxy terminal caspase-recruiting domain (CARD) and		
CC	plays a role in induction of apoptosis. TMS1 gene and protein are useful		
CC	as tools for diagnosing and treating a subject at risk of developing		
CC	cancer (e.g. breast cancer) characterised by abnormal CpG methylation or		
CC	abnormally low levels of TMS1 expression products. Unique fragments of		
CC	TMS1 gene are used as probes. TMS1 gene is useful in gene therapy.		
CC	Increasing TMS1 polypeptide level to an above normal level. The Cpg		
CC	island region of TMS1 or its fragments are used to study the methylation		
CC	patterns apart from any coding region contained in it.		
CC	The present sequence is human target of methylation-induced silencing-1		
CC	(TMS1) exon3 DNA.		
QD	Sequence 356 BP; 85 A; 108 C; 94 G; 69 T; 0 other;		

Query Match	48.1%	Score 356	DB 22	Length 356
Best Local Similarity	100.0%	Pred. No. 2	8e-66	
Matches 356	Conservative 0	Mismatches 0	Indels 0	Gaps 0
QY	385	GCCTGCACCTTATATAGACGACGACCGGGCTGCGCTTATCGCGAGGGCTACAAACGTTGACT	444	
Db	1	GCCTGCACCTTATATAGACGACGACCGGGCTGCGCTTATCGCGAGGGCTACAAACGTTGAGT	60	
QY	445	GGCTGCTGGATGCTCTGTATACGGGAAGGTCCTGACCGGATGACGATACCAAGCAGTGCGGG	504	
Db	61	GGCTGCTGGATGCTCTGTATACGGGAAGGTCCTGACCGGATGACGATACCAAGCAGTGCGGG	120	
QY	505	CCGAGCCCAACCAACCCAGCAAGATGCGGAAAGCTCTCAGTTTCACACCAGCCTGGAACT	564	
Db	121	CCGAGCCCAACCAACCCAGCAAGATGCGGAAAGCTCTCAGTTTCACACCAGCCTGGAACT	180	
QY	565	GGACCTGCAGAGACTTGGTCTCTCCAGGCCCTTAAGGGAAGTCCCAAGTCTCACTGTTGGAGG	624	
Db	181	GGACCTGCAGAGACTTGGTCTCTCCAGGCCCTTAAGGGAAGTCCCAAGTCTCACTGTTGGAGG	240	
QY	625	ACCTGGAACGGAGCTGAGAGCTCTTCCACAGCAACACTCGGGTCAGCCCTGGCAATCCCA	684	
Db	241	ACCTGGAACGGAGCTGAGAGCTCTTCCACAGCAACACTCGGGTCAGCCCTGGCAATCCCA	300	
QY	685	CCAAATCATCCGATCTGATCTTTTATPACCAATATACGAAAAGCCAGCTTGA	740	
Db	301	CCAAATCATCCGATCTGATCTTTTATPACCAATATACGAAAAGCCAGCTTGA	356	

Search completed: December 13, 2002, 08:23:45  
job time : 275 secs

Sequence 356 BP; 85 A; 108 C; 94 G; 69 T; 0 other;

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## SUMMARIES

score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

(million) updates/sec  
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Minimum DB seq length: 0
Maximum DB seq length: 20000000000

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post-processing:	Minimum Match	0%
	Maximum Match	100%

Listing first 45 summaries

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40:	em_higo_mns:*	
41:	em_higo_other:*	

Pred. No. is the number of results predicted by chance to have a

Result						Description
No.	Score	Query	Match	Length	ID	
1	740	100.0	740	6	AX082246	Sequence
2	740	100.0	740	6	AF384665	Homo sapi
3	734	99.2	770	6	AX118619	Sequence
4	734	99.2	770	6	AF184073	Homo sapi
5	734	99.2	782	6	AX459863	Sequence
6	734	99.2	782	9	AB023416	Homo sapi
7	733	99.1	779	6	AX017270	Sequence
8	713	96.4	740	9	AK000211	Homo sapi
9	687	92.8	712	9	AF310103	Homo sapi
10	680	91.9	772	9	BC013569	Homo sapi
11	610	82.4	713	6	AX118641	Sequence
12	610	82.4	713	6	AF255794	Homo sapi
13	585	79.1	385	6	AX082248	Sequence
14	437.6	59.1	768	6	BC004470	Homo sapi
15	378	51.1	405	6	AX118643	Sequence
16	360	48.6	2821	6	AF184072	Sequence
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18	360	48.6	233305	9	AC009088	Homo sapi
19	356	48.1	356	6	AX118626	Sequence
20	336	45.4	732	10	BC008252	Sequence
21	336	45.4	770	10	AB032249	Mus muscu
22	336	45.4	777	6	AX082258	Sequence
23	336	45.4	803	6	AX118637	Sequence
24	333	45.0	701	10	AF310104	Mus muscu
25	322	43.5	626	6	AX118621	Sequence
26	321	43.4	340	6	AX118622	Sequence
27	316.2	42.7	579	6	AX082260	Sequence
28	309.8	41.9	321	6	AX408419	Sequence
29	276.8	37.4	605	6	AB059327	Mus muscu
30	177.8	24.0	1115	10	AB059327	Mus muscu
31	177.8	24.0	71177	2	AC101465	Mus muscu
32	177.8	24.0	191928	2	AC124461	Mus muscu
33	177.8	24.0	225984	2	AC093175	Mus muscu
34	177.6	24.0	551	6	AX459859	Sequence
35	177.6	24.0	551	6	HXMZD548H5	Sequence
36	174.4	23.6	587	6	AF454669	Homo sapi
37	174.4	22.9	807	6	AX048091	Sequence
38	169.4	22.9	270	6	AX117218	Sequence
39	166	22.4	168975	2	AC101629	Rattus no
40	129	15.9	52521	2	AC106629	Mus muscu
41	125.4	15.9	60803	2	AC102309	Mus muscu
42	115	15.5	3419	9	AX026393	Homo sapi
43	115	15.5	4133	9	HSMB00983	Homo sapi
44	115	15.5	4194	6	AX089763	Sequence
45	115	15.5	4200	9	AF229061	Homo sapi

## ALIGNMENTS

RESULT 1				
AX082246				
LOCUS	AX082246	740 bp	DNA	linear
DEFINITION	Sequence 48 from Patent WO0100826.			PAT 27-FEB-2001
ACCESSION	AX082246			
VERSION	AX082246.1	GI:13171007		
KEYWORDS	.			
SOURCE	human.			
ORGANISM	Homo sapiens			
	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
REFERENCE	1 (bases 1 to 740)			
AUTHORS	Bertin,J.			
TITLE	Novel molecules of the card-related protein family and uses thereof			
JOURNAL	Patent: WO 0100826-A 48 04-JAN-2001;			





QY 421 TCAGAGGGGTACAAAGTTGAGTGGCTGTGATGCTGTCTGATGGGAAGTCTTGACGG 480  
 DB 421 TCAGAGGGGTACAAAGTTGAGTGGCTGTGATGCTGTCTGATGGGAAGTCTTGACGG 480  
 QY 481 ATGAGCAGTACAGGAGAGTGGGGCCGAGCCACCAACCAAGCAAGATGCGGAAGCTGT 540  
 DB 481 ATGAGCAGTACAGGAGAGTGGGGCCGAGCCACCAACCAAGCAAGATGCGGAAGCTGT 540  
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 DB 721 ATACGAAGCCAGCTTGAA 740  
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 AX118619  
 LOCUS AX118619 770 bp DNA linear PAT 11-MAY-2001  
 DEFINITION Sequence 2 from Patent WO0129235.  
 ACCESSION AX118619 GI:14035570  
 VERSION AX118619.1  
 KEYWORDS human.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 770)  
 AUTHORS Vertino, P.M.  
 TITLE Tms1 compositions and methods of use  
 JOURNAL Patent: WO 0129235-A 2 26-APR-2001;  
 Emory University (US)  
 FEATURES  
 source  
 location/Qualifiers  
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 /organism="Homo sapiens"  
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 BASE COUNT 157 a 247 c 241 g 125 t  
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 Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 187 TGTCCATGACGCCCTTGACCTTCACCGACACACTGCTGACTTCTACCTGAGACCTACG 246  
 DB 208 TGTCCATGACGCCCTTGACCTTCACCGACACACTGCTGACTTCTACCTGAGACCTACG 267  
 QY 247 GGGCCGAGCTCAACCGCTTAACGCTGCTGCGGACATGGGCGCTGAGAGATGGCGGGGAGC 306  
 DB 268 GGGCCGAGCTCAACCGCTTAACGCTGCTGCGGACATGGGCGCTGAGAGATGGCGGGGAGC 327  
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 QY 487 AGTACCGAGCACTGCGGGCCGAGCCGACCAACCAAGATGCGGAAGCTTTCAGTT 546  
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 QY 547 TCACACACGCGTGAAGTGGAGTGGAGTGGAGTGGTCTCTCCAGGCGCTTAAGGAGTCC 606  
 DB 568 TCACACACGCGTGAAGTGGAGTGGAGTGGAGTGGTCTCTCCAGGCGCTTAAGGAGTCC 627  
 QY 607 AGTCTACCTGTGTGAGAGCACTGAGCGGAGTGGAGTGGTCTCTCCAGCAACACTCCGT 666  
 DB 628 AGTCTACCTGTGTGAGAGCACTGAGCGGAGTGGAGTGGTCTCTCCAGCAACACTCCGT 687  
 QY 667 CAGCCCTGTGCAATCCCAACCAATCATCTGATCTTTTATACCAATATACGA 726  
 DB 688 CAGCCCTGTGCAATCCCAACCAATCATCTGATCTTTTATACCAATATACGA 747  
 QY 727 AAGGCCAGCTTGAA 740  
 DB 748 AAGGCCAGCTTGAA 761  
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 AF184073  
 LOCUS AF184073 770 bp mRNA linear PRI 02-FEB-2001  
 DEFINITION Homo sapiens target of methylation-induced silencing 1 (TMS1) mRNA,  
 complete cds.  
 ACCESSION AF184073  
 VERSION AF184073.1 GI:9863863  
 KEYWORDS  
 SOURCE  
 ORGANISM Homo sapiens.  
 Homo sapiens.  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.  
 REFERENCE 1 (bases 1 to 770)  
 AUTHORS Conway, K.E., McConnell, B.B., Bowring, C.E., Donald, C.D., Warren, S.T.  
 TITLE TMS1, a novel proapoptotic caspase recruitment domain protein, is a  
 target of methylation-induced gene silencing in human breast  
 cancers  
 JOURNAL Cancer Res. 60 (22), 6236-6242 (2000)  
 MEDLINE 20552139  
 PUBMED 11103776  
 REFERENCE 2 (bases 1 to 770)  
 McConnell, B.B. and Vertino, P.M.  
 Activation of a caspase-9-mediated apoptotic pathway by subcellular  
 distribution of the novel caspase recruitment domain protein TMS1  
 Cancer Res. 60 (22), 6243-6247 (2000)  
 JOURNAL MEDLINE 20552140  
 PUBMED 11103777  
 REFERENCE 3 (bases 1 to 770)  
 Vertino, P.M.  
 TITLE Direct Submission



QY 487 AGTACGAGAGTGGCGGGCCGAGCCACCAACCAAGATGCGGAGCTTTCAGTT 546  
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RESULT 6  
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LOCUS  
DEFINITION Homo sapiens ASC mRNA for apoptosis-associated speck-like protein  
ACCESSION AB023416  
VERSION AB023416.2 GI:10801601  
KEYWORDS ASC.  
SOURCE Homo sapiens CDNA to mRNA.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Masumoto,J., Taniguchi,S., Ayukawa,K., Sarvotham,H., Kishino,T.,  
Nikawa,N., Hidaka,E., Katsuyama,T., Higuchi,T. and Sagara,J.  
TITLE A novel 22-kDa protein, aggregates during apoptosis of human  
promyelocytic leukemia HL-60 cells  
J. Biol. Chem. 274 (48), 33835-33838 (1999)  
JOURNAL  
MEDLINE 20036508  
REFERENCE 2 (bases 1 to 782)  
AUTHORS Masumoto,J., Sagara,J. and Taniguchi,S.  
TITLE Direct Submission  
JOURNAL Submitted (04-FEB-1999) Junya Masumoto, Shinshu University School  
of Medicine, Research Center on Aging and Adaptation, Asahi 3-1-1,  
Matsumoto, Nagano 390-8621, Japan  
(E-mail:masumoto@sch.md.shinshu-u.ac.jp, Tel:81-263-37-2723,  
Fax:81-263-37-2724)  
On Oct 14, 2000 this sequence version replaced gi:6482371.  
COMMENT  
Sequence updated (29-Nov-1999).  
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KLFSFPRANWTKDLLQALRESQSYLVEDLERS"

BASE COUNT 158 a 251 c 246 g 127 t  
Query Match 99.2%; Score 734; DB 9; Length 782;

Best Local Similarity 100.0%; Pred. No. 2.2e-106;  
Matches 734; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 67 GCGAGCGCATCTGAGTGGCTGGAGAACCTGACCCCGAGAGCTCAGAACTTCAAC 126  
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Db 100 GCGAGCGCATCTGAGTGGCTGGAGAACCTGACCCCGAGAGCTCAGAACTTCAAC 159  
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QY 127 TGAAGCTGCTGTGCTGCGCTGCGAGGAGGCTACAGGGCGCATCCGCGGGCGGCTGC 186  
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Db 160 TGAAGCTGCTGTGCTGCGCTGCGAGGAGGCTACAGGGCGCATCCGCGGGCGGCTGC 219  
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QY 187 TGTTCATGAGACGCTTTGAGACTCACCAGACAGCTGTCTACCTTGAGAGCTACG 246  
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Db 280 GCGCGGAGCTCAGCGGTAACTGCTGCGGAGCATGGGGCTGAGAGATGGCGGGCAGC 339  
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Db 520 AGTACGAGGAGTGGCGGGCCGAGCCACCAACCAAGCAAGATGCGGAACTTTCAGTT 579  
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Db 640 AGTCCCTACCTGGTGGAGAGGAGCTGGAGGAGCTGAGGCTCTCTCCAGCAACACTCCGGT 699  
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QY 727 AAAGCCAGCTTGAA 740  
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RESULT 7  
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LOCUS  
DEFINITION Sequence 21 from Patent WO947669.  
ACCESSION AX017270  
VERSION AX017270.1 GI:10042188  
KEYWORDS  
SOURCE human.  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE  
AUTHORS Schmitt,A., Specht,T., Dahl,E., Hinzmann,B., Rosenthal,A. and  
Pilarczyk,C.  
TITLE Human nucleic acid sequences from tissue of breast tumors  
Patent: WO 947669-A 21 23-SEP-1999;  
JOURNAL SCHMITT ARMIN (DE); SPECHT THOMAS (DE); DAHL EDGAR (DE); HINZMANN

Mon Dec 16 07:22:15 2002

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Page 6

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      (DB): PILARSKY CHRISTIAN (DE)
      Location/Qualifiers
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        /db_xref="taxon:9606"
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      ORIGIN
Query Match      99.1%; Score 733; DB 6; Length 779;
Best Local Similarity 100.0%; Pred. No. 3.2e-106;
Matches 733; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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      QY  67  GCGACGCGCATCTGAGATGCGCTGAGAACTTGACCGCGGAGAGCTCAAGAAAGTTCAAGC
      b  107  GCGACGCGCATCTGAGATGCGCTGAGAACTTGACCGCGGAGAGCTCAAGAAAGTTCAAGC
      QY  127  TGAAGCTGCTGCGGCGCGCTGCGGCGGCTCAAGGCGCATCCCGCGGCGCGCGCTGC
      Db  167  TGAAGCTGCTGCGGCGCGCTGCGGCGGCTCAAGGCGCATCCCGCGGCGCGCGCTGC
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      QY  247  GCGCGGACGCTCAACGCTTAACGCTGCGGCGGACATGCGGCGGACATGCGGCGGACG
      Db  287  GCGCGGACGCTCAACGCTTAACGCTGCGGCGGACATGCGGCGGACATGCGGCGGACG
      QY  307  TGCAGGCGGCGCACAGCAGCAGGCGCTGAGACCGCGGCGGACATGCGGCGGACG
      Db  347  TGCAGGCGGCGCACAGCAGCAGGCGCTGAGACCGCGGCGGACATGCGGCGGACG
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      QY  727  AAAGCCAGCTTGA 739
      Db  767  AAAGCCAGCTTGA 779

RESULT 8
AK000211      740 bp      mRNA      linear      PRI 22-FEB-2000
LOCUS      Homo sapiens cDNA FLJ20204 fls, clone COLF1505.
DEFINITION      AK000211
ACCESSION      AK000211.1 GI:7020146
VERSION      oligo capping; fls (full insert sequence).
KEYWORDS
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OY	434	AAACGTTGAGTGGCTGCTGATGCTCTAGCGGGAAGTCTCGTAGCGAGTAGACATACC	493
Db	419	AAACGTTGAGTGGCTGCTGATGCTCTAGCGGGAAGTCTCGTAGCGAGTAGACATACC	478
OY	494	GGCAGTGGCGGCGCAGGCCCAACCAACCAAGCAAGATGCGGGAAGCTCTTCAGTTTCACACC	553
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DEFINITION	AFJ10103 Homo sapiens PYCARD mRNA, complete cds.
ACCESSION	AFJ10103
VERSION	AFJ10103.1 GI:11096298
KEYWORDS	
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo. 1 (bases 1 to 712)
REFERENCE	Martinson,F., Hofmann,K. and Tschopp,J. The Pryn domain: a possible member of the death domain-fold family implicated in apoptosis and inflammation Curr. Biol. 11 (4), R118-R120 (2001) 2 (bases 1 to 712) Martinson,F., Hofmann,K. and Tschopp,J. Direct Submission Submitted (28-SEP-2000) Institute of Biochemistry, University of Lausanne, CH des Boveresses 155, Epalinges 1066, Switzerland
AUTHORS	
TITLE	
JOURNAL	
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BASE COUNT	166 a         221 c         210 g         115 t
ORIGIN	

QY	54	ATGGGGCGCGGGCGGAGAGCCATCTTGGATGCGCTGGAGAAACCTGACCGCGGAGAGGTC	113
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OY	114	AAGAAGTTCAAGCTGAACCTGTGTCGGGTGGCGGCTGCGAGAGGGCTTACGGGCGATCCG	173
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OY	174	CGGGGCGGCGCTGCTGTCCATGGAGCGCCTTGGACNCTCACCGCAACAGCTGGTCAAGCTTTCAC	233
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OY	234	CTGGAGACCTTACGGCGCGGAGAGCTACCGGCTAACGCTGCTCGCGGACATGGGCGCTGCAGAG	293
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OY	294	ATGGCGGGGGCAGCTGTCAGAGCGGGCCACCGACCAAGGGCTTGGAGCGCGGCCAGCTGAGATC	353
Db	241	ATGGCGGGGGCAGCTGTCAGAGCGGGCCACCGACCAAGGGCTTGGAGCGCGGCCAGCTGAGATC	300
OY	354	CAGGCGCCCTCTCTCACTGCGGAGCCCAAGCCAGGCGCTTGACTTATPAGACACAGCCGGGCT	413
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OY	414	GCGCTTATCGGAGGGGTACAAACGTTGAGTGGCTGTGATGCTCTGTACGGGAAGGTC	473
Db	361	GCGCTTATCGGAGGGGTACAAACGTTGAGTGGCTGTGATGCTCTGTACGGGAAGGTC	420
OY	474	CTGACGAGTGAAGCAGTACCAGGCAAGTGGGGCCGAGCCACCACCAAGCAAGATGGCG	533
Db	421	CTGACGAGTGAAGCAGTACCAGGCAAGTGGGGCCGAGCCACCACCAAGCAAGATGGCG	480
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Db	541	CTAAGGAGTCCAGATCTTACCTGGTGGAGAGCCTGGAGCGAGGTGAGGCTCCTTCCCA	600
OY	654	GCAACACTCGCGTCAAGCCCTGGCAATCCCAACCAATCATCCTGAAATCTGATCTTTTAT	713
Db	601	GCAACACTCGCGTCAAGCCCTGGCAATCCCAACCAATCATCCTGAAATCTGATCTTTTAT	660
OY	714	ACACATATATACGAAAGCCAGGCTTGA 740	
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RESULT	10
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DEFINITION	Homo sapiens, apoptosis-associated speck-like protein containing a CARD, clone MGC:8873 IMAGE:3902319, mRNA, complete cds.
ACCESSION	BC013569
VERSION	BC013569.1 GI:15488878
KEYWORDS	MGC.
SOURCE	Homo sapiens.
ORGANISM	Homo sapiens.
REFERENCE	Eukaryotes; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. 1 (bases 1 to 772)
AUTHORS	Strausberg,R.
TITLE	Direct Submission
JOURNAL	Submitted (04-SEP-2001) National Institutes of Health, Mammalian Gene Collection (MGC), Cancer Genomics Office, National Cancer Institute, 31 Center Drive, Room 11A03, Bethesda, MD 20892-2590, USA
REMARK	NIH-MGC project URL: http://mgc.nci.nih.gov
COMMENT	Contact: MGC help desk Email: gcapbs-remail.nih.gov Tissue Procurement: ATCC DNA Library Preparation: Life Technologies, Inc.

cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LINTL)  
DNA Sequencing by: Sequencing Group at the Stanford Human Genome  
Center, Stanford University School of Medicine, Stanford, CA 94305  
Web site: <http://www-shgc.stanford.edu>  
Contact: (Dickson, Mark) [modexall@stanford.edu](mailto:modexall@stanford.edu)  
Dickson, M., Schmutz, J., Grimwood, J., Rodriguez, A., and Myers,  
J. M.

Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/URL at: <http://image.llnl.gov>  
Series: IRAK Plate: 14 Row: c Column: 22  
This clone was selected for full length sequencing because it passed the following selection criteria: matched mRNA gi: 7020146.  
Location/Qualifiers

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	100.00	772	772

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OY	121	TC	AAGCTGAAAGCTGCTGTGCGATTCCGCTCCGCGGAGGGCTACGGGGCGATCCGCGGGGGCG	180
Db	61	TC	AAGCTGAAAGCTGCTGTGCGATTCCGCTCCGCGGAGGGCTACGGGGCGATCCGCGGGGGCG	120
OY	181	CG	CTCTCTCCATGAGCGGCTTGGACTTCACCGACCAAGCTGATGAGCTTCTACTCTGAGAGA	240
Db	121	CG	CTCTCTCTCCATGAGCGGCTTGGACTTCACCGACCAAGCTGATGAGCTTCTACTCTGAGAGA	180
OY	241	CC	TACGCGCGCCGAGCTACCGCTTAACCTGCTGGCCGACATGAGGCGCTGCGAGAGATGAGCGG	300
Db	181	CC	TACGCGCGCCGAGCTACCGCTTAACCTGCTGGCCGACATGAGGCGCTGCGAGAGATGAGCGG	240
OY	301	GG	CAGCTGCAGGGGCGGCACGCGCACAGGGGCTCTGGAGCGCGGCGACAGCTGGGGAATCAGAGGCC	360
Db	241	GG	CAGCTGCAGGGGCGGCACGCGCACAGGGGCTCTGGAGCGCGGCGACAGCTGGGGAATCAGAGGCC	300
OY	361	CT	CCCTCAGTCGCGAGCGCAAGCGAGGCGCTGACCTTATATAGACGACACCGGGCTGGGGCTTAA	420
Db	301	CT	CCCTCAGTCGCGAGCGCAAGCGAGGCGCTGACCTTATATAGACGACACCGGGCTGGGGCTTAA	360
OY	421	TC	CGGAGGGGGTCACAAACCTGTAGTGGGCTGCTGGATGCTCTGTACGGGAAGTCTCTGACGG	480
Db	361	TC	CGGAGGGGGTCACAAACCTGTAGTGGGCTGCTGGATGCTCTGTACGGGAAGTCTCTGACGG	420
OY	481	AT	AAGAGAGTACCAAGCGCAGTGGCGGGCCAGGCCACCAACCTCAGCAAGATTCGCGGAAGCTCT	540
Db	421	AT	AAGAGAGTACCAAGCGCAGTGGCGGGCCAGGCCACCAACCTCAGCAAGATTCGCGGAAGCTCT	480
OY	541	TC	AGTTTCACACCAAGCTGGAACGTGACCTGCAAGAGCATTGGTCTCTTCACAGGCCCTCAAGGG	600

Db	481	TCATTTTACACACAGCCTGGAACTGGACCTGCAGAGACTTCTCTCCAGGCCCTTAAGG	540
Qy	601	AGTCCCACTCTTACCTCGTGTGGAGACCTGGAGCTGAGGCTCTTCCAGCAACAC	660
Db	541	AGTCCCACTCTTACCTCGTGTGGAGACCTGGAGCTGAGGCTCTTCCAGCAACAC	600
Qy	661	TCGGGTAGCCCCCTGGCAATCCCAACCAATCATCTGTGATCTGTTTTATACCAAT	720
Db	601	TCGGGTAGCCCCCTGGCAATCCCAACCAATCATCTGTGATCTGTTTTATACCAAT	660
Qy	721	ATACGAAAGCCAGCTTGAA	740
Db	661	ATACGAAAGCCAGCTTGAA	680

RESULT 11				
LOCUS	AX118641			
DEFINITION	AX118641	713 bp	DNA	linear
ACCESSION	AX118641	24	from Patent WO0129255.	
VERSION	AX118641.1	GI:14035592		
KEYWORDS	human.			
SOURCE	human.			

REFERENCE  
AUTHORS  
TITLE  
JOURNAL

Eukaryota: Chordata: Craniata: Vertebrata: Euteleostomi;  
Mammalia: Eutheria: Plimates: Catarrhini, Homnidae; Homo.  
1 (bases 1 to 713)  
Vertino, P. M.  
Tms1 compositions and methods of use  
Patent: WO 0129235-A 24 26-APR-2001;  
Emory University (US)

[illegible]

Query Match	82.4%;	Score 610;	DB 6;	Length 713;
Best Local Similarity	92.2%;	Pred. No. 7.8e-87;		
Matches 677; Conservative	0;	Mismatches	0;	Indels 57; Gaps 1-

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187	TGTCCTGAGAGCGCTTGAGACCTACGACGAAACCTGTCACTTCTACCTGGAGACTAGC	246
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247	GGCGCGAGGTCACCGCTAAACGTGCTGCGCGACATGGGCTGCTACGAGAAATGGCGGGGACGC	306
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QY      667 CAGCCCCCTGGCAATCCCAACCAATCATCTGATCTGATCTTTATACCAATATACGA 726
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DEFINITION Homo sapiens target of methylation-induced silencing-1 (TMS1) mRNA, complete cds, alternatively spliced.
ACCESSION AF255794
VERSION   AF255794.1 GI:9802275
KEYWORDS
SOURCE   Homo sapiens.
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.
REFERENCE
AUTHORS Conway K.E., McConnell B.B., Bowring C.E., Donald C.D., Warren S.T.
and Vertino P.M.
TITLE TMS1, a novel proapoptotic caspase recruitment domain protein, is a target of methylation-induced gene silencing in human breast cancers
JOURNAL Cancer Res. 60 (22), 6243-6247 (2000)
PUBMED 2052139
REFERENCE
AUTHORS McConnell B.B. and Vertino P.M.
TITLE Activation of a caspase-9-mediated apoptotic pathway by subcellular redistribution of the novel caspase recruitment domain protein TMS1
JOURNAL Cancer Res. 60 (22), 6243-6247 (2000)
PUBMED 2052140
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Best Local Similarity 92.2%; Pred. No. 7.8e-87;
Matches 677; Conservative 0; Mismatches 0; Indels 57; Gaps 1;

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[illegible][illegible]



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DEFINITION	Sequence 26 from Patent WO0129235.	405 bp	DNA	linear	PAT 11-MAY-2001
ACCESSION	AX118643				
VERSION	AX118643.1	GI:14035594			
KEYWORDS					
SOURCE	human.				
ORGANISM	Homo sapiens				

REFERENCE	AUTHORS	TITLE	JOURNAL
1 (pages 1 to 405)	Vertino, P. M.	Tmsl compositions and methods of use	Patent: WO 0129235-A 26 26-APR-2001;
			Emory University (US)

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URES      Location/Qualifiers
source     1..405
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            /db_xref="taxon:9606"
CDS        75..>404
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Query Match	51.18;	Score 378;	DB 6;	Length 405;
Best Local Similarity	100.0%;	Pred. No. 3e-50;		
Matches 378; Conservative	0;	Mismatches	0;	Indels 0; Gaps 0;

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Job time : 2839 secs

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[illegible]

ACCESSION	BW926438
VERSION	BM926438.1
KEYWORDS	EST.
SOURCE	human.
ORGANISM	Homo sapiens
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
TITLE	1 (Bases 1 to 804)
JOURNAL	NIH-MGC http://mgc.nci.nih.gov/. National Institutes of Health, Mammalian Gene Collection (MGC) Unpublished (1999)
COMMENT	Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: Life Technologies, Inc. CDNA Library Preparation: Life Technologies, Inc. CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Agencourt Bioscience Corporation Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: http://image.llnl.gov Plate: LLM12824 row = a column= 15 High quality sequence stop: 746. Location/Qualifiers 1..804 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:5766806" /clone.lib="NIH_MGC_122" /lab.host="DH10B" /note="Organ: pooled lung and spleen; Vector: pCMV-Sport6; Site: 1: NotI; Site 2: EcoRV (destroyed); RNA source: anonymous pool of 24 week female lung, 16 week female spleen, and 20-22 week male spleens. Library is oligo-dT primed, and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.4 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 026. Note this is a NIH-MGC library."
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 SOURCE human.  
 ORGANISM Homo sapiens  
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 1 (bases 1 to 856)  
 NIH-MGC http://mgi.nci.nih.gov/  
 National Institutes of Health, Mammalian Gene Collection (MGC)  
 Unpublished (1999)  
 Contact: Robert Strausberg, Ph.D.  
 Email: cgaphs@email.nih.gov  
 Tissue Procurement: ATCC/DCTD/DTF  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
 http://image.llnl.gov  
 Plate: LICM1745 row: e column: 05  
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 GGCAGAG(G). Size-selected >500bp for average insert size  
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 of Gerald M. Rubin (University of California, Berkeley)  
 using ZAP-cDNA synthesis kit (Stratagene) and Superscript  
 II RT (Life Technologies). Note: this is a NIH\_MGC  
 library."

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Query Match 93.4%; Score 690.8; DB 12; Length 856;  
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DEFINITION	mRNA sequence.				
ACCESSION	BG337806.1 GI:13144342				
VERSION	EST.				
KEYWORDS	human.				
SOURCE	Homo sapiens				
ORGANISM	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
REFERENCE	Mammalia; Euthera; Primates; Catarrhini; Hominoidea; Homo.				
AUTHORS	N.I. (bases 1 to 748)				
TITLE	NIH-MGC http://mgc.nci.nih.gov/.				
JOURNAL	National Institutes of Health, Mammalian Gene Collection (MGC)				
COMMENT	Unpublished (1999) Contact: Robert Strausberg, Ph.D. Email: cgabbs-remail.nih.gov Tissue Procurement: ATCC CDNA Library Preparation: Ling Hong/Rubin Laboratory CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Incyte Genomics, Inc. Clone distribution: MCC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: ILICM1251 row: b column: 03 High quality sequence stop: 710. Location/Qualifiers 1..748 /organism="Homo sapiens" /db_xref="taxon:9606" /clone="IMAGE:455378" /clone_1lb="NIH_MGC_46" /tissue_type="telomysarcoma cell line" /lab_host="DH10B (phage-resistant)" /note="Organ: uterus; Vector: pORF7, Site 1: XhoI; Site 2: EcoRI; CDNA made by oligo(dT) priming. Alternatively cloned into EcoRI/XhoI sites selected following 5' adaptor: GGGCAGAG(6). Size-selected >500bp for average insert size 1.8kb. Library consists of approximately 10^6 clones from the laboratory of Gerald R. Rubin (University of California, Berkeley) using 2AP-CDNA synthesis kit (Stratagene) and Superscript II RT (Life Technologies). Note: this is a NIH_MGC library."				
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OY	435	AACGTTAGAGGCTGCTGATGCTCTGTACGGGAAGGCTCTGCACGGATGAGCAGTACCG	494	
Db	422	AACGTTAGAGGCTGCTGATGCTCTGTACGGGAAGGCTCTGCACGGATGAGCAGTACCG	481	
OY	495	GCAGTGCGGGCCAGGCCACCACAAACCAAGCAAGAATGGCGAAGGCTCTTCAATTTCACACCA	554	
Db	482	GCAGTGCGGGCCAGGCCACCACAAACCAAGCAAGAATGGCGAAGGCTCTTCAATTTCACACCA	541	
OY	555	GCTCGAATGTGACCTCGCAAGGACTTGTCTCTCCAGGCCCTTAAGGAGATGCCAGTCTAC	614	
Db	542	GCTCGAATGTGACCTCGCAAGGACTTGTCTCTCCAGGCCCTTAAGGAGATGCCAGTCTAC	601	
OY	615	CTGTGGAGAGACCTGTGAGCGGAGCTGAGGCTCTCTCCAGAACACTCGGCTACGCCCC-	673	
Db	602	CTGTGGAGAGACCTGTGAGCGGAGCTGAGGCTCTCTCCAGAACACTCGGCTACGCCCC	661	
OY	674	TGGCAATCCCAACCAATCATCTGATCTGATCTTTTATACACATATACGAAGAAGCA	733	
Db	662	TGTCATATCCCAACCAATCATCTGATCTGATCTTATATACACATATATACGAAGAAGCA	720	
OY	734	GCTTGA 740		
Db	721	GCTTGA 727		
RESULT 8				
LOCUS	A114855/c	678 bp	mRNA	linear EST 28-OCT-1998
DEFINITION	A114855.x1	g688g10.x1	Scapens-placenta_8tc9weeks_2nbhp8to9w	Homo sapiens cDNA sequence
ACCESSION	U014855.1	GI:3677027		
VERSION	1			
KEYWORDS	BST			
SOURCE	Human			
ORGANISM	Homo sapiens			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;			
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.			
TITLE	Nci-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.			
JOURNAL	National Cancer Institute, Cancer Genome Anatomy Project (CGAP).			
COMMENT	Tumor Gene Index Unpublished (1997)			
FEATURES	Contact: Robert Strausberg, Ph.D. Email: cgaps-r@email.nih.gov This clone is available royalty-free through LNLN ; contact the IMAGE Consortium (info@image.llnl.gov) for further information. Insert Length: 804 Std Error: 0.00 Seq primer: -40ml3 fwd. ET from Amersham High quality sequence stop: 402. Location/Qualifiers 1..678 /organism="Homo sapiens" /db_xref="taxon:9606" /clone_lib="IMAGE:1714818" /clone_lib="Soares-placenta_8tc9weeks_2nbhp8to9w" /dev_stage="two placentaes: one from 8 weeks and another from 9 weeks post conception" /lab_host="DH10B (ampicillin resistant)" /note="Organ: placenta; Vector: pTZ19D (Pharmacia) with a modified polylinker; Site 1: Not I; Site 2: Eco RI; Site 3: Hind III; double-stranded cDNA was size selected, ligated into adapters (Pharmacia), digested with Not I, ligated into the Not I and Eco RI sites of a modified pTZ19 vector (Pharmacia). Library constructed by Benito Soares and			



BASE COUNT 114 a 202 c 217 g 145 t  
 ORIGIN

Query Match 90.6%; Score 670.4; DB 9; Length 678;  
 Best Local Similarity 99.9%; Pred. No. 4.3e-131;  
 Matches 671; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

69 GAGGCATCTGATGGCGTGGAGAACCTACCGCCGAGAGCTCAAGAGTTCAAGCTG 128  
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 Db 678 GAGGCATCTGATGGCGTGGAGAACCTACCGCCGAGAGCTCAAGAGTTCAAGCTG 619

129 AACCTGCTGCGTGGCGCTGCGGAGGAGCTACGGGCGCATCCGCGGGGCGCTGCTG 188  
 |||  
 Db 618 AACCTGCTGCGTGGCGCTGCGGAGGAGCTACGGGCGCATCCGCGGGGCGCTGCTG 559

189 TCATGAGAGCGCTTGGACCTTACCGACAGCTGGTCACTTCACTTGAAGACCTTACGGC 248  
 |||  
 Db 558 TCATGAGAGCGCTTGGACCTTACCGACAGCTGGTCACTTCACTTGAAGACCTTACGGC 499

249 GCGGAGCTACCGCTTACCGTGGCGGAGATGGGCTGAGAGAGATGGCGGGCAGCTG 308  
 |||  
 Db 498 GCGGAGCTACCGCTTACCGTGGCGGAGATGGGCTGAGAGAGATGGCGGGCAGCTG 439

309 CAGGCGGCGACGACGAGGAGCTGAGAGCGCGCAGCTGGATCCAGGCGCCCTCTCAG 368  
 |||  
 Db 438 CAGGCGGCGACGACGAGGAGCTGAGAGCGCGCAGCTGGATCCAGGCGCCCTCTCAG 379

369 TCGGACCGACAGCGAGGCTGCACTTTATAGACAGCAGCGGCGCTTATCGCGAGG 428  
 |||  
 Db 378 TCGGACCGACAGCGAGGCTGCACTTTATAGACAGCAGCGGCGCTTATCGCGAGG 319

429 GTACACAACGTTAGTGGCTGCTGATGCTCTGTACGCGGAAGTCTTACAGGATGACAG 488  
 |||  
 Db 318 GTACACAACGTTAGTGGCTGCTGATGCTCTGTACGCGGAAGTCTTACAGGATGACAG 259

489 TACCAGGACATGGGCGCGGAGCCACCAACCAAGAGATGGGAGAGCTTTCAGTTTC 548  
 |||  
 Db 258 TACCAGGACATGGGCGCGGAGCCACCAACCAAGAGATGGGAGAGCTTTCAGTTTC 199

549 ACAACGACCTGGAACCTGGACCTGCAAGGACTTCTCTCCAGGCGCTTAAAGGAGTCCAG 608  
 |||  
 Db 198 ACAACGACCTGGAACCTGGACCTGCAAGGACTTCTCTCCAGGCGCTTAAAGGAGTCCAG 139

609 TCTTACTGCTGGAGAGACCTGGAGCGGAGCTGAGGCTCTTCCAGCAACATCCGGTCA 668  
 |||  
 Db 138 TCTTACTGCTGGAGAGACCTGGAGCGGAGCTGAGGCTCTTCCAGCAACATCCGGTCA 79

669 GCCCCTGGCAATCCACCAATCATCTGATCTTTTATACATATACGAAA 728  
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 Db 78 GCCCCTGGCAATCCACCAATCATCTGATCTTTTATACATATACGAAA 19

729 AGCCAGCTTGA 740  
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 Db 18 AGCCAGCTTGA 7

RESULT 9  
 BM051141 741 bp mRNA linear EST 07-NOV-2001  
 LOCUS 603614063F1 NIH\_MGC\_43 Homo sapiens cDNA clone IMAGE:5424590 5',  
 DEFINITION mRNA sequence.  
 ACCESSION BM051141  
 VERSION BM051141.1 GI:16780408  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.  
 REFERENCE 1 (bases 1 to 741)  
 AUTHORS NIH-MGC <http://mgc.nci.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)

COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: ATCC  
 cDNA Library Preparation: Ling Hong/Rubin Laboratory  
 cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: LLCMI885 Row: n Column: 15  
 High quality sequence stop: 643.  
 Location/Qualifiers  
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 /organism="Homo sapiens"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:5424590"  
 /clone\_lib="NIH\_MGC\_43"  
 /tissue\_type="normal pigmented retinal epithelium"  
 /lab\_host="DH10B (phage-resistant)"  
 /note="Organ: eye; Vector: pOT7; Site\_1: XhoI; Site\_2:  
 EcoRI; cDNA made by oligo-dT priming. Directionally  
 cloned into EcoRI/XhoI sites using the following 5'  
 adaptor: GGCACGAG(G). Library constructed by Ling Hong  
 in the laboratory of Gerald M. Rubin (University of  
 California, Berkeley) using ZAP-cDNA synthesis kit  
 (Stratagene) and Superscript II RT (Life Technologies).  
 Note: this is a NIH\_MGC library. |"

BASE COUNT 139 a 243 c 237 g 122 t  
 ORIGIN

Query Match 90.2%; Score 667.6; DB 13; Length 741;  
 Best Local Similarity 97.1%; Pred. No. 1.7e-130;  
 Matches 701; Conservative 0; Mismatches 19; Indels 2; Gaps 2;

7 CGGCTGACGGGGGTGAGCGCGGACGCGCGGGAGTCTTGAGACCATGGCGCGCGC 66  
 |||  
 Db 21 CGGCTGACGGGGGTGAGCGCGGACGCGCGGGAGTCTTGAGACCATGGCGCGCGC 80

67 GCGACCGCATCTTGATGCGCTGGAGAACTGACCGCGGAGAGCTTAACAAGTTCAAGC 126  
 |||  
 Db 81 GCGACCGCATCTTGATGCGCTGGAGAACTGACCGCGGAGAGCTTAACAAGTTCAAGC 140

127 TGAAGCTGCTGGGTGCGCTGCGGAGGAGCTACGGGCGCATCCGCGGGGCGCTGC 186  
 |||  
 Db 141 TGAAGCTGCTGGGTGCGCTGCGGAGGAGCTACGGGCGCATCCGCGGGGCGCTGC 200

187 TGTTCATGAGACGCTTGACCTACCGACAAGTGTGACGCTTCTACCTGAGACCTACG 246  
 |||  
 Db 201 TGTTCATGAGACGCTTGACCTACCGACAAGTGTGACGCTTCTACCTGAGACCTACG 260

247 GCGCGGAGCTCACCGCTTAACGCTGCGGACATGGGCTTGCAGAGATGGCGGGGAGC 306  
 |||  
 Db 261 GCGCGGAGCTCACCGCTTAACGCTGCGGACATGGGCTTGCAGAGATGGCGGGGAGC 320

307 TGCAGGCGGCGACGACACAGGAGCTGAGAGCGGCGGACGCTGGAGATCCAGGCCCTTC 366  
 |||  
 Db 321 TGCAGGCGGCGACGACACAGGAGCTGAGAGCGGCGGACGCTGGAGATCCAGGCCCTTC 380

367 AGTCGAGCGCAAGCCAGGCGCTGACTTTATAGACAGCAGCGGCTGCGCTTATCGCGA 426  
 |||  
 Db 381 AGTCGAGCGCAAGCCAGGCGCTGACTTTATAGACAGCAGCGGCTGCGCTTATCGCGA 440

427 GGGTCACAAACGTTGAGTGGCTGCTGATGCTCTGTACGGGAAGTCTTACGAGATGAGC 486  
 |||  
 Db 441 GGGTCACAAACGTTGAGTGGCTGCTGATGCTCTGTACGGGAAGTCTTACGAGATGAGC 500

487 AGTACGAGGAGTGGCGGCGGAGCGCCACCAACCAAGCAAGATGGGAGCTCTTCAGTT 546  
 |||  
 Db 501 AGTACGAGGAGTGGCGGCGGAGCGCCATACCAACCAAGATGGGAGCTCTTCAGTT 560

547 TCACACGAGCGCTGGAAGCTGCAAGAGACTTGTCTCTCAAGGCGCTTAAGGAGTCCC 606  
 |||  
 Db 561 TCACACGAGCGCTGGAAGCTGCAAGAGACTTGTCTCTCAAGGCGCTTAAGGAGTCCC 620



cdna library Preparation: Life Technologies, Inc.  
 cdna library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM9704 row: j column: 16  
 High quality sequence stop: 660.

## FEATURES

source

Location/Qualifiers

1..675

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:3902319"

/clone\_lib="NIH\_MGC\_70"

/tissue\_type="epithelial carcinoma"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: pancreas; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally. Primer: Oligo dT.  
 Average insert size 1.1 kb. Library constructed by Life  
 Technologies."

BASE COUNT 151 a 214 c 198 g 112 t  
 ORIGIN

Query Match

Best Local Similarity 99.5%; Score 654.2; DB 12; Length 675;

Matches 656; Conservative 0; Mismatches 3; Indels 0; Gaps 0;

## FEATURES

source

Location/Qualifiers

1..744

/organism="Homo sapiens"

/db\_xref="taxon:9606"

/clone="IMAGE:4476088"

/clone\_lib="NIH\_MGC\_91"

/tissue\_type="adenocarcinoma, cell line"

/lab\_host="DH10B (phage-resistant)"

/note="Organ: prostate; Vector: pCMV-SPORT6; Site:1: NotI;  
 Site:2: SalI; Cloned unidirectionally; oligo-dT primed.  
 Average insert size 1.4 kb. Library enriched for  
 full-length clones and constructed by Life Technologies.  
 Note: this is a NIH\_MGC Library."

BASE COUNT 159 a 227 c 238 g 120 t  
 ORIGIN

Query Match

Best Local Similarity 97.0%; Score 647.4; DB 12; Length 744;

Matches 713; Conservative 0; Mismatches 16; Indels 6; Gaps 5;

QY 82 ATGCGCTGAGAACTGAGCCGCCGAGAGCTCAAGATTCAAGTCAAGCTGTCGG 141  
 DB 1 ATGCGCTGAGAACTGAGCCGCCGAGAGCTCAAGATTCAAGTCAAGCTGTCGG 60  
 QY 142 TGGCGCTGGCGAGGGCTACGGGCGCATCCGGGGGGCGGCTGCTCATGAGAGCCT 201  
 DB 61 TGGCGCTGGCGAGGGCTACGGGCGCATCCGGGGGGCGGCTGCTCATGAGAGCCT 120  
 QY 202 TGGAGCTCAACGACAGCTGTGCTTACCTGAGAGACTAGGCGCGAGCTCAGCG 261  
 DB 121 TGGAGCTCAACGACAGCTGTGCTTACCTGAGAGACTAGGCGCGAGCTCAGCG 180  
 QY 262 CTAAAGTGTGCGGAGATGGGCTGAGAGATGGCGGGGAGCTGCAAGGCGGACGC 321  
 DB 181 CTAAAGTGTGCGGAGATGGGCTGAGAGATGGCGGGGAGCTGCAAGGCGGACGC 240  
 QY 322 ACCAGGCTGTGAGCGCGGCGAGTGGATCCAGGCGCTCTCATGTCGGAGCCAGC 381  
 DB 241 ACCAGGCTGTGAGCGCGGCGAGTGGATCCAGGCGCTCTCATGTCGGAGCCAGC 300  
 QY 382 CAGGCTGTGACTTATAGACACAGACCGGGCTGCTTATCGGAGGGTCAAAAGCTTG 441  
 DB 301 CAGGCTGTGACTTATAGACACAGACCGGGCTGCTTATCGGAGGGTCAAAAGCTTG 360  
 QY 442 AGTGGCTGTGATGCTGTACGAGGAGGCTCTGACGGATGAGTACAGGAGGAGTG 501  
 DB 361 AGTGGCTGTGATGCTGTACGAGGAGGCTCTGACGGATGAGTACAGGAGGAGTG 420  
 QY 502 GGGCGAGGCGCAACCAACCAAGATAGGAGAGCTCTTCACTTCAACACAGCTTGA 561  
 DB 421 GGGCGAGGCGCAACCAACCAAGATAGGAGAGCTCTTCACTTCAACACAGCTTGA 480  
 QY 562 ACTGAGCTGCAAGAGCTGTCTTCAGAGCCCTTAAGGAGTCCAGTCTTACTGTTG 621  
 DB 481 ACTGAGCTGCAAGAGCTGTCTTCAGAGCCCTTAAGGAGTCCAGTCTTACTGTTG 540  
 QY 622 AGGAGCTGAGGAGGAGCTGAGGCTCTTCCAGCAACACTCGGTCAGGCGCTGGCAATC 681  
 DB 541 AGGAGCTGAGGAGGAGCTGAGGCTCTTCCAGCAACACTCGGTCAGGCGCTGGCAATC 600  
 QY 682 CCACCAATCATCTGAAATCTGATCTTTATACAAATATAGAAAGCCAGCTTGAA 740  
 DB 601 CCACCAATCATCTGAAATCTGATCTTTATACAAATATAGAAAGCCAGCTTGAA 659

RESULT 12

BG255521  
 LOCUS BG255521 744 bp mRNA linear EST 13-FEB-2001  
 DEFINITION 602367671F1 NIH\_MGC\_91 Homo sapiens cdna clone IMAGE:4476088 5',  
 mRNA sequence.  
 ACCESSION BG255521  
 VERSION BG255521.1 GI:12765259  
 KEYWORDS EST.  
 SOURCE human.  
 ORGANISM Homo sapiens  
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.  
 REFERENCE 1 (bases 1 to 744)  
 AUTHORS NIH-MGC <http://imgc.ncl.nih.gov/>.  
 TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
 JOURNAL Unpublished (1999)  
 COMMENT Contact: Robert Strausberg, Ph.D.  
 Email: [cgapbs-remail.nih.gov](mailto:cgapbs-remail.nih.gov)  
 Tissue Procurement: DCTD/DRP  
 cdna library Preparation: Life Technologies, Inc.  
 DNA Sequencing by: Incyte Genomics, Inc.  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: L1AM10302 row: m column: 17  
 High quality sequence stop: 661.

QY 8 GCGTCGAGCGGGGTGAGCGCGGAGCGCGGGGATCTGAGAGCCATGAGGCGCGCGG 67  
 DB 1 GCGTCGAGCGGGGTGAGCGCGGAGCGCGGGGATCTGAGAGCCATGAGGCGCGCGG 60  
 QY 68 CGAGGCTATCTGATGCGTGGAGAACTGACCGCGGAGAGCTCAAGAGTTCAAGCT 127  
 DB 61 CGAGGCTATCTGATGCGTGGAGAACTGACCGCGGAGAGCTCAAGAGTTCAAGCT 120  
 QY 128 GAAGCTGTGCTGCGTCCCGTGGCGAGGCTACGGGGCGATCCGCGGGCGCGCTGCT 187  
 DB 121 GAAGCTGTGCTGCGTCCCGTGGCGAGGCTACGGGGCGATCCGCGGGCGCGCTGCT 180  
 QY 188 GTCCATGAGAGGCTTGGAGCTTACCGCAAGAGTGTACAGCTTCTTACTGGAGACTACG 247  
 DB 181 GTCCATGAGAGGCTTGGAGCTTACCGCAAGAGTGTACAGCTTCTTACTGGAGACTACG 240  
 QY 248 CGCGGAGCTACCGCTTACAGTGTGCGGACATGAGGCTTGCAGAGAGATGGCGGAGCT 307  
 DB 241 CGCGGAGCTACCGCTTACAGTGTGCGGACATGAGGCTTGCAGAGAGATGGCGGAGCT 300  
 QY 308 GGAAGGCGGCGAGCAACAGGCTGAGGCGCGGAGCTGGAGATCCAGGCGCGCTCTCA 367  
 DB 301 GGAAGGCGGCGAGCAACAGGCTGAGGCGCGGAGCTGGAGATCCAGGCGCGCTCTCA 360  
 QY 368 GTGCGGAGCCAAAGCCAGGCTGTGACTTATAGACGACACCGGGGCTGCGCTTATCCGAG 427  
 DB 361 GTGCGGAGCCAAAGCCAGGCTGTGACTTATAGACGACACCGGGGCTGCGCTTATCCGAG 420

OY	428	GATCACAACCTTTAGTGGCTGCTGTGATGCTGTGTCACGGAAGTGCTCGACGATGACCA	487
Db	421	GGTCCAAACCTTTAGTGGCTGCTGTGATGCTGTGTCACGGAAGTGCTCGACGATGACCA	480
OY	488	GTACCAGGCACTGGCGGCCGACGCCACCAACCAACCAAGATGACGAGACTCTTCACATT	547
Db	481	GTACCAGGCACTGGCGGCCGACGCCA-CAACCCAGCAAGATGACGAGACTCTTCACATT	539
OY	548	CACACCAAGCCCTGGAACCTGCAAGGACTTGTCTCTCCAGGCCCTTAAGGAGTCCCA	607
Db	540	CACACCAAGCCCT-GAACTGGACCTGCAAGGACTTGTCTCTCCAGS-CTTAAGGAGTCCCA	597
OY	608	GTCTTACCTGTGGAGAGCACTGGAGCGAGCTGAGCTCTTCCAGCAACACTCCGCTC	667
Db	598	GTCTTACCTGTGGAGAGCACTGGAGCGAGCTGAGCT-CTTCCAGCAACACTCCGCTC	656
OY	668	AGCCCCCTGGCAATCCCAAAATCATCTGAAAT--CTGATCTTTTATACCAATATATACG	725
D	657	AGCCCCGGGAATATCCCACAAAATATCTGATTTCTGATCTTTTATACCAATATATACG	716
OY	726	AAAAAGCCAGCTTGAA 740	
Db	717	AAAAAGCCAGTTGAAA 731	
RESULT 13			
LOCUS	BE909218	687 bp mRNA linear EST 20-OCT-2000	
DEFINITION	60150147BF1 NIH_MGC_70 Homo sapiens cDNA clone IMAGE:3903498 5',		
ACCESSION	BE909218	mRNA sequence.	
VERSION	BE909218.1	GI:10404770	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	NIH-MGC http://mgs.nci.nih.gov/		
JOURNAL	Unpublished (1999)		
COMMENT	National Institutes of Health, Mammalian Gene Collection (MGC) Contact: Robert Strausberg, Ph.D. Email: cgabs@emall.nih.gov Tissue Procurement: ATCC cDNA Library Preparation: Life Technologies, Inc. cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL) DNA Sequencing by: Incyte Genomics, Inc. Clone Distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a> Plate: LLAM9707 row: k column: 19 High quality sequence stop: 673. Location/Qualifiers		
FEATURES			
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	/clone.lib="NIH_MGC_70"		
	/tissue.type="epithelioid carcinoma"		
	/lab.host="DH10B (phage-resistant)"		
	/note="Organ: pancreas; Vector: pCMV-Sport6; Site:1; NotI; Site:2; SalI; Cloned unidirectionally. Primer: Oligo dP. Average insert size 1.1 kb. Library constructed by Life Technologies."		
BASE COUNT	140 a 219 c 214 g 114 t		
ORIGIN			
Query Match	86.4%; Score 639; DB 12; Length 687;		
Matches Local Similarity	98.7%; Pred.No. 1-7e-14;		
Batches 676; Conservative	0; Mismatches 5; Indels 4; Gaps 3;		
OY	48	GGAGCCATGGGGGGCGCGGCGGACGCCCAATCCGTGATCGCTGGAGAACCTGACCCGCCA	60
Db	1	GGAGCCATGGGGGGCGCGGCGGACGCCCAATCCGTGATCGCTGGAGAACCTGACCCGCCA	60
OY	107	GGAGCTCAAAAGATTTCAAGCTGAAGTGTGTGCGGTGCGCGGCGGCAAGGCTACAGGGC	166
Db	61	GGAGCTCAAAAGATTTCAAGCTGAAGTGTGTGCGGTGCGCGGCGGCAAGGCTACAGGGC	120
OY	167	CATCCCGCGGGCGCGCTGTCGCATGGAAGCCCTTGGACCTCACCAAGGTGTGAC	226
Db	121	CATCCCGCGGGCGCGCTGTCGCATGGAAGCCCTTGGACCTCACCAAGGTGTGAC	180
OY	227	CTTCTACCTGGAACCTACAGGCGAGCTCACCGCTTAACGTGTGCGCAACTGTGGCCT	286
Db	181	CTTCTACCTGGAACCTACAGGCGAGCTCACCGCTTAACGTGTGCGCAACTGTGGCCT	240
OY	287	GCAGAGATGAGCGGGCAGCTCAGCGGCCACGACCAAGGCTCTTGAGCCCGCGAC	346
Db	241	GCAGAGATGAGCGGGCAGCTCAGCGGCCACGACCAAGGCTCTTGAGCCCGCGAC	300
OY	347	TGGATATCAGAGCCCTCTCTCAGTGGGACGCCAAGGCAAGGCTGTATATACCAAGCA	406
Db	301	TGGATATCAGAGCCCTCTCTCAGTGGGACGCCAAGGCAAGGCTGTATATACCAAGCA	360
OY	407	CCGGGCTGCGCTTATCGCAGAGGTACAAACCTTAGTGGTGTGTGATCTCTGACG	466
Db	361	CCGGGCTGCGCTTATCGCAGAGGTACAAACCTTAGTGGTGTGTGATCTCTGACG	420
OY	467	GAAAGTCTGACGATGAGAGTACAGGAGTGGCGGCGCAGCCCAACCAAGCA	526
Db	421	GAAAGTCTGACGATGAGAGTACAGGAGTGGCGGCGCAGCCCAACCAAGCA	480
OY	527	GATCGGAACTCTTATGATTTACACACAGCCCTGAACTGACCTGCAAGAGACTTGTCT	586
Db	481	GATCGGAACTCTTATGATTTACACACAGCCCTGAACTGACCTGCAAGAGACTTGTCT	540
OY	587	CCAGGCCCTTAAGGAGATCCAGCTCTACTGTTGGAGACTGGAGCGAGCTGAGGCTC	646
Db	541	CCAGGCCCTTAAGGAGATCCAGCTCTACTGTTGGAGACTGGAGCGAGCTGAGGCTC	600
OY	647	CTTCCCGACCAACTCCGGTCCAGCCCTGGCAATCCCAAAATCATCTGATGTGANC	706
Db	601	-TTCCCGACCAACTCCGGTCCAGCCCTGG-ATACTCCAAATCATCTGATGTGANC	657
OY	707	TTTTATACCAATATACGAAAAGC 731	
Db	658	TTTTATACCAATATACGAAAAGC 682	
RESULT 14			
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DEFINITION	UT-H-DT1-awc-P-21-0-UI-s1 NCI CGAP-DT1 Homo sapiens cDNA clone		
ACCESSION	BM998354	IMAGE:5887748 3', mRNA sequence.	
VERSION	BM998354.1	GI:19723255	
KEYWORDS	EST.		
SOURCE	human.		
ORGANISM	Homo sapiens		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
AUTHORS	Mammalia; Eutheria; Primates; Catarrhini; Homidae; Homo.		
TITLE	NCI CGAP http://www.ncbi.nlm.nih.gov/ncicgap		
JOURNAL	Unpublished (1997)		
COMMENT	National Cancer Institute, Cancer Genome Anatomy Project (CGAP), Tumor Gene Index Unpublished (1997) Contact: Robert Strausberg, Ph.D. Email: cgabs@emall.nih.gov Tissue Procurement: Dr. Jose Mercuende cDNA Library Preparation: Dr. M. Bento Soares, University of Iowa cDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Clone distribution information can be found through the I.M.A.G.E. Consortium/LNL at: <a href="http://image.llnl.gov">http://image.llnl.gov</a>		



Mon Dec 16 07:22:19 2002

us-09-728-721-48.rst

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    |||||
OY 367 AGTCGCGAGCCAGCAGCAGGCGTCTGTGAGCCGCCAGCTGSGATCCAGGCCCTCCTC 426
    |||||
Db 336 -----GGCCTGCACCTTATAGACCAGCACCGGGCTGGCTTATCGCGA 378
    |||||
OY 427 GGTTCACAAAGCTTGTGAGTGTGCTGTGATGCTCTGTACGGGAAGTCTGTACGGATGAGC 486
    |||||
Db 379 GGTTCACAAAGCTTGTGAGTGTGCTGTGATGCTCTGTACGGGAAGTCTGTACGGATGAGC 438
    |||||
OY 487 AGTACCGAGGAGTGTGCGGCGCGAGCCAGCACAACCCAGCAAGATGCGGAAGCTCTTCAGTT 546
    |||||
Db 439 AGTACCGAGGAGTGTGCGGCGCGAGCCAGCACAACCCAGCAAGATGCGGAAGCTCTTCAGTT 498
    |||||
OY 547 TCACACAGGCTGTGAATGTGACCTGTCAAGGACTTGTCTCCAGGCCCTTAAGGAGTCCC 606
    |||||
Db 499 TCACACAGGCTGTGAATGTGACCTGTCAAGGACTTGTCTCCAGGCCCTTAAGGAGTCCC 558
    |||||
OY 607 AGTCTACCTGTGTGAGGAGCCTGTGAGCGGAGCTGTGAGGCTCTTCCAGCAACACTCCGTT 666
    |||||
Db 559 AGTCTACCTGTGTGAGGAGCCTGTGAGCGGAGCTGTGAGGCTCTTCCAGCAACACTCCGTT 618
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OY 667 CAGCCCGCTGGCAATCCCAACCAATCATCTGAAATCTGATCTTTTATACAAATATACGA 726
    |||||
Db 619 CAGCCCGCTGGCAATCCCAACCAATCATCTGAAATCTGATCTTTTATACAAATATACGA 678
    |||||
OY 727 AAAGCCAGCTTGA 740
    |||||
Db 679 AAAGCCAGCTTGA 692
    |||||
```

Search completed: December 13, 2002, 09:48:55  
Job time : 2175 secs



Db	121	TCAMGCTGAAGCTGCTGTGTGGTCCGCTGGCCGAGAGGGCTACAGGGGGCATTCGCCGGGGGCG	180
QY	181	CGCGTCGTGTCATGAGGACGCTGTGGACCTGCACAGCAAACTGGTACGCTTCTACTGAGAGA	240
Db	181	CGCTGCTGTCTCATGAGAGGCTTGGACCTGCACAGCAAGCTGGTACGCTTCTACTGAGAGA	240
QY	241	CTTACGCGCCCGCACTCACCCGTAACTGCTGGCCACATGGGCTCTGCAGAGATGGCCG	300
Db	241	CTTACGCGCCCGCACTCACCCGTAACTGCTGGCCACATGGGCTCTGCAGAGATGGCCG	300
QY	301	GGCAGCTGCAGGGGGCCACGACACCAAGGACTCTGAGACCCGCGCAGCTGGGATCCAGGCC	360
Db	301	GGCAGCTGCAGGGGGCCACGACACCAAGGACTCTGAGACCCGCGCAGCTGGGATCCAGGCC	360
QY	361	CTCTCAGTGGGAGCAAGCCAGGCGCTGCACCTTATAGACAGCAGCAGGCGCTCCGCTTA	420
Db	361	CTCTCAGTGGGAGCAAGCCAGGCGCTGCACCTTATAGACAGCAGCAGGCGCTCCGCTTA	420
Y	421	TCGCGAGGGGTCAACAAACGCTTGAAGTGGCTGGTGGATCTCTGTACGGGAAGGCTCTGACG	480
Db	421	TCGCGAGGGGTCAACAAACGCTTGAAGTGGCTGGTGGATCTCTGTACGGGAAGGCTCTGACG	480
QY	481	ATGAGCAGTACACAGCAGTGGGGGCGACGCCACCAACCCAGCAAGATGCGGAAGCTCT	540
Db	481	ATGAGCAGTACACAGCAGTGGGGGCGACGCCACCAACCCAGCAAGATGCGGAAGCTCT	540
QY	541	TCAGTTTCAACACAGCTGGAACTGAGACTGAGCAAGAGCTTGCTCTCCAGGCGCTTAAGG	600
Db	541	TCAGTTTCAACACAGCTGGAACTGAGACTGAGCAAGAGCTTGCTCTCCAGGCGCTTAAGG	600
QY	601	AGTCCAGTCTTACCTGGTGGAGAGACCTGGAGGGGAGCTGAGGCTCTCCACAGCAAC	660
Db	601	AGTCCAGTCTTACCTGGTGGAGAGACCTGGAGGGGAGCTGAGGCTCTCTCCACAGCAAC	660
QY	661	TCGGGTACGCCCCCTGGCAATCCCAACCAATCATCTGAACTTGAACTTTATATACAAAT	720
Db	661	TCGGGTACGCCCCCTGGCAATCCCAACCAATCATCTGAACTTGAACTTTATATACAAAT	720
QY	721	ATATGAAAGGCCAGCTTGAA	740
Db	721	ATATGAAAGGCCAGCTTGAA	740
RESULT 2			
US-09-996-617-7			
Sequence 7, Application US/09996617			
Patent No. US20020128198A1			
GENERAL INFORMATION:			
APPLICANT: Berlin, John			
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED			
FILE OF INVENTION: PROTEIN FAMILY AND USES THEREOF			
FILE REFERENCE: 07334-340001			
CURRENT APPLICATION NUMBER: US/09/996,617			
CURRENT FILING DATE: 2001-11-27			
PRIOR APPLICATION NUMBER: 09/931,071			
PRIOR FILING DATE: 2001-08-15			
PRIOR APPLICATION NUMBER: 09/428,252			
PRIOR FILING DATE: 1999-10-27			
PRIOR APPLICATION NUMBER: 09/340,620			
PRIOR FILING DATE: 1999-06-28			
NUMBER OF SEQ ID NOS: 10			
SOFTWARE: FastSeq for Windows Version 4.0			
SEQ ID NO 7			
LENGTH: 740			
TYPE: DNA			
ORGANISM: Homo sapiens			
FEATURES:			
NAME/KEY: CDS			
LOCATION: (34)...(638)			
US-09-996-617-7			

	Best Local Similarity	100.0%	Pred.	No. 3e-172:	
	Matches	740;	Conservative	0;	Mismatches 0; Indels 0; Gaps 0;
OY	1	CGCGTCGGGCTGCACAGCGGGGTGAAGCGGGGCCACGCGCCGGGGATCCTGGAGCATGGGC	60		
Dd	1	CGCGTCCGGGTGAGCGGGGTGAAGCGGGGCCACGCGCCGGGGATCCTGGAGCATGGGC	60		
OY	61	GCGCGCGCAGCCCATCTCGATGCGCTGCGTAGAACCTTGACC GCCGAGAGCTCAACAAGT	120		
Dd	61	GCGGCGCCGAGCCATCTCGATGCGCTGCGTAGAACCTTGACC GCCGAGAGCTCAACAAGT	120		
OY	121	TCAAAGTGAAGCTGTGTGTGGTGCCGCTGCACGAGGCGTAAAGGGCCATCCCGGGGGCG	180		
Dd	121	TCAAAGCTGAAGCTGTGTGTGGTGCCGCTGCACGAGGCGTAAAGGGCCATCCCGGGGGCG	180		
OY	181	CGCGTGTGTTCATGAGAGGCGCTTGAGACTTCACGAAAGCTGATAGCTTCTAAGTTGAGA	240		
Dd	181	CGCGTGTGTTCATGAGAGGCGCTTGAGACTTCACGAAAGCTGATAGCTTCTAAGTTGAGA	240		
OY	241	CCTTGGGCGCGGAGCTCACCGCTTAACGTCGTCGCGAGACATGGGCGTTGACAGAGATGGCG	300		
Dd	241	CCTTGGGCGCGGAGCTCACCGCTTAACGTCGTCGCGAGACATGGGCGTTGACAGAGATGGCG	300		
OY	301	GCGAGCTGCAGGCGGCGACGACCAAGGCGCTGGAGCGCGCGCCAGCTGGGGATCCAGGCC	360		
Dd	301	GCGAGCTGCAGGCGGCGACGACCAAGGCGCTGGAGCGCGCGCCAGCTGGGGATCCAGGCC	360		
OY	361	CTCTCGATGTGGGAGCAAGCAGGCGCTTCATTATAGACACAGACCGGGCTGCGCTTA	420		
Dd	361	CTCTCGATGTGGGAGCAAGCAGGCGCTTCATTATAGACACAGACCGGGCTGCGCTTA	420		
OY	421	TCGGGAGGCTTCATAAACCTTGAGTGGCTGTCTGTGATCTCTGTACGGGAAGTCTTGAGG	480		
Dd	421	TCGGGAGGCTTCATAAACCTTGAGTGGCTGTCTGTGATCTCTGTACGGGAAGTCTTGAGG	480		
OY	481	ATGAGCAGTATCCAGGCAATGCGGGCGGAGCCACCAACCAAGCAAGATGGCGAAGCTCT	540		
Dd	481	ATGAGCAGTATCCAGGCAATGCGGGCGGAGCCACCAACCAAGCAAGATGGCGAAGCTCT	540		
OY	541	TCAATTTCAACACAGCCTTGGAACCTGAGCCTGCAGAAGACTTGTCTTCACAGGCCCTTAAGG	600		
Dd	541	TCAATTTCAACACAGCCTTGGAACCTGAGCCTGCAGAAGACTTGTCTTCACAGGCCCTTAAGG	600		
OY	601	AGTCCCAGTCTTACCTGATGTGAGACACTGAGAGCGGAGAGCTGAGGCTCTCTCCAGCAAC	660		
Dd	601	AGTCCCAGTCTTACCTGATGTGAGACACTGAGAGCGGAGAGCTGAGGCTCTCTCCAGCAAC	660		
OY	661	TCGCGTCAGCCCCCTGGCAATCCACCAANTATCTTAATCTATCTTTTTATACAAAT	720		
Dd	661	TCGCGTCAGCCCCCTGGCAATCCACCAANTATCTTAATCTATCTTTTTATACAAAT	720		
OY	721	ATACGAAAAGCCAGCTTGAA	740		
Dd	721	ATACGAAAAGCCAGCTTGAA	740		
<b>RESULT 3</b>					
US-09-996-617-10/C					
; sequence 10, Application us/09996617					
; Patent No. US200720128198A1					
; GENERAL INFORMATION:					
APPLICANT: Bertin John					
TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED					
FILE REFERENCE: 0734-540001					
CURRENT FILING DATE: 2001-11-27					
PRIORITY APPLICATION NUMBER: US/09/996, 617					
PRIOR FILING DATE: 2001-08-15					
PRIOR APPLICATION NUMBER: 09/428, 252					
PRIOR FILING DATE: 1999-10-27					
PRIOR APPLICATION NUMBER: 09/340, 620					
PRIOR FILING DATE: 1999-06-28					



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; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 10
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-996-617-10
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Query Match          100.0%; Score 740; DB 10; Length 740;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGGCGAGCGCCGGGATCCTGGAGCCATGGGCG 60
DB 740 CGCGTCCGGCTGACAGCGGGGTGAGCGCGGCGAGCGCCGGGATCCTGGAGCCATGGGCG 681
QY 61 GCGCGCGGCGAGCCATCCTGGATGCGGCTGAGAGAACCTGACCCCGAGAGCTCAAGAACT 120
DB 680 GCGCGCGGCGAGCCATCCTGGATGCGGCTGAGAGAACCTGACCCCGAGAGCTCAAGAACT 621
QY 121 TCAAGCTGAAGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 180
DB 620 TCAAGCTGAAGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 561
QY 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACAGCTGCTCACTTCTACTTGAGAGA 240
DB 560 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACAGCTGCTCACTTCTACTTGAGAGA 501
QY 241 CCTACGGCGCGGAGCTACCGCTTAACGTCTGCGGACACATGAGGCGCTGACAGAGATGGCG 300
DB 500 CCTACGGCGCGGAGCTACCGCTTAACGTCTGCGGACACATGAGGCGCTGACAGAGATGGCG 441
QY 301 GGCAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 440 GGCAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 381
QY 361 CTCCTCAGTCGCGAGCGCAAGCGCTTGAACCTTATAGCAGCAGCGGCGTGCCTTA 420
DB 380 CTCCTCAGTCGCGAGCGCAAGCGCTTGAACCTTATAGCAGCAGCGGCGTGCCTTA 321
QY 421 TCGCGAGGGGTCAACAAAGTTGAGTGGCTGCTGATCTCTGTAACGGGAAGTCTTGACGG 480
DB 320 TCGCGAGGGGTCAACAAAGTTGAGTGGCTGCTGATCTCTGTAACGGGAAGTCTTGACGG 261
QY 481 ATGAGCAGTACAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 260 ATGAGCAGTACAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 201
QY 541 TCAGTTTTCACACAGCCTGGAAGTGAAGTCTGCAAGGACTTGTCTCCAGGCGCTTAAGGG 600
DB 200 TCAGTTTTCACACAGCCTGGAAGTGAAGTCTGCAAGGACTTGTCTCCAGGCGCTTAAGGG 141
QY 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
DB 140 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 81
QY 661 TCCGGTCAAGCCCTGCGCATCCCAACAATCATCTGATCTGATCTTTTATACAAAT 720
DB 80 TCCGGTCAAGCCCTGCGCATCCCAACAATCATCTGATCTGATCTTTTATACAAAT 21
QY 721 ATACGAAAAGCCAGCTTGAA 740
DB 20 ATACGAAAAGCCAGCTTGAA 1
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RESULT 4
US-09-841-879B-4
; Sequence 4, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
; FILE REFERENCE: 07334-330001
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; CURRENT APPLICATION NUMBER: US/09/841.879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 4
; LENGTH: 740
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (54)...(638)
US-09-841-879B-4
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Query Match          100.0%; Score 740; DB 10; Length 740;
Best Local Similarity 100.0%; Pred. No. 3e-172;
Matches 740; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGGCGAGCGCCGGGATCCTGGAGCCATGGGCG 60
DB 1 CGCGTCCGGCTGACAGCGGGGTGAGCGCGGCGAGCGCCGGGATCCTGGAGCCATGGGCG 60
QY 61 GCGCGCGGCGAGCCATCCTGGATGCGGCTGAGAGAACCTGACCCCGAGAGCTCAAGAACT 120
DB 61 GCGCGCGGCGAGCCATCCTGGATGCGGCTGAGAGAACCTGACCCCGAGAGCTCAAGAACT 120
QY 121 TCAAGCTGAAGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 180
DB 121 TCAAGCTGAAGCTGCTGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCGTCG 180
QY 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACAGCTGCTCACTTCTACTTGAGAGA 240
DB 181 CGCTGCTGTCATGAGACGCTTGAACCTCACCAGACAGCTGCTCACTTCTACTTGAGAGA 240
QY 241 CCTACGGCGCGGAGCTACCGCTTAACGTCTGCGGACACATGAGGCGCTGACAGAGATGGCG 300
DB 241 CCTACGGCGCGGAGCTACCGCTTAACGTCTGCGGACACATGAGGCGCTGACAGAGATGGCG 300
QY 301 GGCAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
DB 301 GGCAGCTGAGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 360
QY 361 CTCCTCAGTCGCGAGCGCAAGCGCTTGAACCTTATAGCAGCAGCGGCGTGCCTTA 420
DB 361 CTCCTCAGTCGCGAGCGCAAGCGCTTGAACCTTATAGCAGCAGCGGCGTGCCTTA 420
QY 421 TCGCGAGGGGTCAACAAAGTTGAGTGGCTGCTGATCTCTGTAACGGGAAGTCTTGACGG 480
DB 421 TCGCGAGGGGTCAACAAAGTTGAGTGGCTGCTGATCTCTGTAACGGGAAGTCTTGACGG 480
QY 481 ATGAGCAGTACAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
DB 481 ATGAGCAGTACAGCAGAGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGGCGG 540
QY 541 TCAGTTTTCACACAGCCTGGAAGTGAAGTCTGCAAGGACTTGTCTCCAGGCGCTTAAGGG 600
DB 541 TCAGTTTTCACACAGCCTGGAAGTGAAGTCTGCAAGGACTTGTCTCCAGGCGCTTAAGGG 600
QY 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
DB 601 AGTCCAGTCTTACCTGCTGAGAGACCTGAGCGGAGCTGAGGCTCTCCAGCAACAC 660
QY 661 TCCGGTCAAGCCCTGCGCATCCCAACAATCATCTGATCTGATCTTTTATACAAAT 720
DB 661 TCCGGTCAAGCCCTGCGCATCCCAACAATCATCTGATCTGATCTTTTATACAAAT 720
QY 721 ATACGAAAAGCCAGCTTGAA 740
DB 721 ATACGAAAAGCCAGCTTGAA 740
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Query	March	Similarity	79.1%;	Score	585;	DB	10;	Length	585;
Best	Local	Similarity	100.0%;	Pred.	No. 2.3e-134;				
Matches	585;	Conservative	0;	Mismatches	0;	Indels	0;	Gaps	0;

  

QY	54	ATGGGGCGCGCGCGCGAGCCCATCTGGATCGCGTGGAGAACTGACCGCCGAGGAGCTC	113
	1	ATGGGGCGCGCGCGCGAGCCCATCTGGATCGCGTGGAGAACTGACCGCCGAGGAGCTC	60
QY	114	AAGAAGTTCAAAGCTGAAGCTGCTGTGCGTGCCTGCGCGAGGGGCTATCGGCGCATCCCG	173
	61	AAGAAGTTCAAAGCTGAAGCTGCTGTGCGTGCCTGCGCGAGGGGCTATCGGCGCATCCCG	120
QY	174	CGGGGCGCGCTGCTGTCCATGAGAGCCCTTGGACCTCAACGGAAGCTGTGAGCTTCTAC	233
	121	CGGGGCGCGCTGCTGTCCATGAGAGCCCTTGGACCTCAACGGAAGCTGTGAGCTTCTAC	180
QY	234	CTGAGAGACTTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATAGGGGCTGCGAGAG	293
	181	CTGAGAGACTTACGGCGCGAGCTCACCGCTTAACGTGCTGCGGACATAGGGGCTGCGAGAG	240
QY	294	ATTGGCCGGGCGAGCTGCGAGGGCGGCCACGACCAAGGGCTTTGGAGCCGCGCCAGCTGGATC	353
	241	ATTGGCCGGGCGAGCTGCGAGGGCGGCCACGACCAAGGGCTTTGGAGCCGCGCCAGCTGGATC	300
QY	354	CAGGCCCCCTCTCAAGTGGGAGCCAAAGCCAGAGCCCTGCACTTTATGAGCAGAGACGGGCT	413
	301	CAGGCCCCCTCTCAAGTGGGAGCCAAAGCCAGAGCCCTGCACTTTATGAGCAGAGACGGGCT	360
QY	414	GCAGCTTATCGGAGGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAGGTC	473
	361	GCAGCTTATCGGAGGGGTCAACAAAGTTGAGTGGCTGCTGATGCTCTGTACGGGAGGTC	420
QY	474	CTGACGATGAGCACTACCAAGCAGTGGGGCCGACCCACCAACCAAGCAAGATGGCG	533

Query Match	Best Local Similarity	79.1%;	Score 585;	DB 10;	Length 585;
Matches	585;	Conservative	0;	Mismatches	0;
				Indels	0;
				Gaps	0;
QY	54	ATGGGGCGCGCGCGCGAGCCCATCTGGATGCGCTGGAGAACCTGACGGCGAGAGCTC	113		
Db	1	ATGGGGCGCGCGCGCGAGCCCATCTGGATGCGCTGGAGAACCTGACGGCGAGAGCTC	60		
QY	114	AAGAAGTTCAGAGCTCAAGCTGCTGTGCGGAGCGCGCGAGGGGCTACGGGGGCAATCCG	173		
Db	61	AAGAAGTTCAGAGCTCAAGCTGCTGTGCGGAGCGCGCGAGGGGCTACGGGGGCAATCCG	120		
QY	174	CGGGGCGCGCTGCTGTCCATGGAGCGCCTTGGACCTCACCGACAGCTGTCAAGCTTCTAC	233		
Db	121	CGGGGCGCGCTGCTGTCCATGGAGCGCCTTGGACCTCACCGACAGCTGTCAAGCTTCTAC	180		
QY	234	CTGGAGACTCTAAGGCGCGAGAGCTCAACCGCTAACGCTGCTCGGACATGSGGCTGCAGAG	293		
Db	181	CTGGAGACTCTAAGGCGCGAGAGCTCAACCGCTAACGCTGCTCGGACATGSGGCTGCAGAG	240		
QY	294	ATGCGCGGGCAGACTGCGAGCGCGGCACGCAACAGGGCTCTGGAGCGCGCAGCTGGGATC	353		
Db	241	ATGCGCGGGCAGACTGCGAGCGCGGCACGCAACAGGGCTCTGGAGCGCGCAGCTGGGATC	300		
QY	354	CAGGCGCCCTCTCAAGTCGGGACGCAAGGCGAGGCTCTGATTAATGAGCAGGACCGGGCT	413		
Db	301	CAGGCGCCCTCTCAAGTCGGGACGCAAGGCGAGGCTCTGATTAATGAGCAGGACCGGGCT	360		
QY	414	GCGCTTATCGCGAGGGGTACAAACGTTGAGTGGCTGTGGATGCTCTGTACGGGAAGTC	473		
Db	361	GCGCTTATCGCGAGGGGTACAAACGTTGAGTGGCTGTGGATGCTCTGTACGGGAAGTC	420		
QY	474	CTGAGGATGAGCAATTAACAGGCAATGGGGGCGGAGGCCACGACCAACCAAGCAAGATGGG	533		
Db	421	CTGAGGATGAGCAATTAACAGGCAATGGGGGCGGAGGCCACGACCAACCAAGCAAGATGGG	480		
QY	534	AAGCTCTTCAGTTTACACCAAGCTTGGAACTTGAACTTGAAAGGACTTGTCTCTCAAGGCC	593		



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; PRIOR APPLICATION NUMBER: US 09/207,359
; PRIOR FILING DATE: 1998-12-08
; PRIOR APPLICATION NUMBER: US 09/099,041
; PRIOR FILING DATE: 1998-06-17
; PRIOR APPLICATION NUMBER: US 09/019,942
; PRIOR FILING DATE: 1998-02-06
; NUMBER OF SEQ ID NOS: 71
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 60
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)...(667)
US-09-728-721-60
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Query Match          45.4%; Score 336; DB 10; Length 777;
Best Local Similarity 72.9%; Pred. No. 2e-73;
Matches 461; Conservative 0; Mismatches 165; Indels 6; Gaps 2;
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18 GGGTGAACGCGGCGACCGCGGGGATCTGAGCCATGGGCGCGCGCGACGCCATC 77
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 GAGTAAAGGTGACCGCGGCTGCCACCCAGAGCCATGGGCGCGCGAGATGCCATC 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
78 CTGGATGCGCTGGAGACCTGACCGCGCGAGAGCTCAAGAGTTCAAGCTGAGCTGCTG 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
113 CTGGAGCGCTCTTAAACTTGTACAGGAGATGAACCTAATAAGTTCAAGATGAAGCTGCTG 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
138 TCGGTGCGCGTGGCGAGGAGCTACGGGCGCATCCCGGGGCGCGCTGTCTCATGAGAC 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
173 ACAGTCACTGCGAGAAAGCTATGGGCGCATCCACGCGGGGCGCTGTCTCATGAGAC 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
198 GCCTTGACCTCAACCAAGCTGTGACCTTACTTGAAGACTCAAGGCGCGGAGCTC 257
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
233 GCCATGATCTCACTGACAACTGTACACTACTATCTGAGAGTGTATGGCTTGGAGCTC 292
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
258 ACCGCTAACGTGCTGGCGACATGGGCTGACAGAGATGGCGGGAGCTGACAGGCGCC 317
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
293 ACATGACTGTGCTTGAAGACATGGGCTTACAGAGACTGTGCTGACAGCTGCAAGC--- 349
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
318 ACGCACCAGGCGCTGAGAGCGCGCGAGCTGGGATCCAGGCGCGCTCTCATGAGAGCC 377
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
350 ACTAAGAGAGAGCTGAGACTGTGGAGCTGAGCGAGCTGCTCTCATGAGATACAGCC 409
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
378 AAGCCAGGCGCTGACTTATAGACCAAGCGCGCTGCGCTTATCCGAGAGCTCAACAAC 437
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
410 AGAACAGG---ACACTTTGTGGACACAGCAAGGCAAGCACTCATTTGCCAGGGTACAGAA 466
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
438 GTTGAAGTGGCTGTGATGCTGTGACGGGAAGTCTCTGACGATGAGAGTACAGAGCA 497
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
467 GTGGAGAGAGTGTGATGCTTTCATGAGAGTGTGCTGACTGATAGAGAGTACAGAGCA 526
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
498 GTGCGGGCGAGCGCAACCAAGCAAGAGTGGAGAGCTTTCAGTTTCAACAGAGCC 557
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
527 GTTCGTGACAGAGCAACAGCAAGCAAGATGAGAGCTTTCAGTTTGTTCATCC 586
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
558 TGAAGTGAAGCTGCAAGAGCTGCTCTCCAGAGCTTGAAGAGAGTCCAGTCTCATCTG 617
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
587 TGAAGCTGACCTGCAAGAGCTCTCTCCAGAGCTTGAAGAGAAATACATCTCTCTG 646
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
618 GTGAGAGACTGAGCGGAGCTGAGAGCTCTT 649
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
647 GTGATGAGCTGAGAGAGCTGAGATCTT 678
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 12
US-09-841-879B-1
; Sequence 1, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
; TITLE OF INVENTION: NOVEL MOLECULES OF THE CARD-RELATED PROTEIN FAMILY AND USES THERE
```

```
; FILE REFERENCE: 07334-330001
; CURRENT APPLICATION NUMBER: US/09/841,879B
; CURRENT FILING DATE: 2001-04-24
; PRIOR APPLICATION NUMBER: US 09/728,721
; PRIOR FILING DATE: 2000-12-01
; PRIOR APPLICATION NUMBER: US 09/340,620
; PRIOR FILING DATE: 1999-06-28
; NUMBER OF SEQ ID NOS: 19
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 777
; TYPE: DNA
; ORGANISM: Mus musculus
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (89)...(667)
US-09-841-879B-1
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Query Match          45.4%; Score 336; DB 10; Length 777;
Best Local Similarity 72.9%; Pred. No. 2e-73;
Matches 461; Conservative 0; Mismatches 165; Indels 6; Gaps 2;
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   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
53 GAGTAAAGGTGACCGCGGCTGCCACCCAGAGCCATGGGCGCGCGAGATGCCATC 112
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
78 CTGGATGCGCTGGAGACCTGACCGCGAGAGCTCAAGAGTTCAAGCTGAGAGCTGCTG 137
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
113 CTGGAGCGCTCTTAAACTTGTACAGGAGATGAACCTAATAAGTTCAAGATGAAGCTGCTG 172
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
138 TCGGTGCGCGTGGCGAGGAGCTACGGGCGCATCCCGGGGCGCGCTGTCTCATGAGAC 197
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
173 ACAGTCACTGCGAGAAAGCTATGGGCGCATCCACGCGGGGCGCTGTCTCATGAGAC 232
   ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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RESULT 13
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; Sequence 18, Application US/09841879B
; Patent No. US20020142979A1
; GENERAL INFORMATION:
; APPLICANT: Berlin, John
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FILE REFERENCE: 44921-5028-WO  
CURRENT APPLICATION NUMBER: US/09/880,107  
CURRENT FILING DATE: 2001-06-14  
PRIOR APPLICATION NUMBER: US 60/211,379  
PRIOR FILING DATE: 2000-06-14  
PRIOR APPLICATION NUMBER: US 60/237,054  
PRIOR FILING DATE: 2000-10-02  
NUMBER OF SEQ ID NOS: 3950  
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US-09-880-107-1066

Query Match 41.9%; Score 309.8; DB 10; Length 321;  
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Job time : 65 secs

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